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ABSTRACT

Student knowledge in a subject area prior to and after instruction has traditionally been assessed by administering a pre- and post-test, usually multiple choice, though recent studies criticize the use of even the best-constructed multiple choice tests. This study assessed college freshmen's knowledge before and after a laboratory experience in molecular genetics, based on results from pre- and post-lab clinical interviews and multiple choice tests. The specific areas addressed by this research were: (1) students' misconceptions and missing concepts in molecular genetics as revealed by interviews; (2) changes in student comprehension and knowledge as a result of laboratory instruction as revealed by interviews; (3) student scores on both multiple choice tests and interview tasks; and (4) discrepancies found between knowledge expressed on multiple choice tests versus interviews. Study results indicated that interviews were effective in revealing student misconceptions and missing concepts and that the amount of data generated by interviews was substantially greater than information gained from multiple choice test scores on student comprehension of concepts in molecular genetics. Concept maps are included and appendices contain the test instruments and interview transcripts of representative students. (ML)

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A SMALL-SCALE INTERVIEW STUDY OF COLLEGE FRESHMEN'S KNOWLEDGE OF CONCEPTS, PRINCIPLES AND PROCESSES IN MOLECULAR GENETICS BEFORE AND AFTER LABORATORY INSTRUCTION

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Introduction

Student knowledge in a particular subject area prior to and after instruction has traditionally been assessed by administering a pre- and post-test, usually multiple choice. This method has been used both in educational research and in teaching.The rationale behind the use of such tests is that the results are amenable to quantification, and relatively large numbers of students can be processed at one time. Pre-tests are generally used to assess current student knowledge in a subject matter and as indicators of where instructional emphasis should be placed.

Multiple choice tests are in wide use in education, despite the general recognition that items for such tests are difficult to construct if they are meant to reveal comprehension. Numerous studies have shown that even the best-constructed multiple choice tests contain a high proportion of items that require mere factual recall by the student (See J.T. Robinson, 1979, for review). Recently, Novak and Gowin (1984) criticized the use of objective pencil-and-paper tests to assess student knowledge, both in educational research and in classroom practice. Their research, based on the learning theory of Ausubel (1968), makes a distinction between rote and meaningful learning, and emphasizes educational research and teaching methods that reveal meaningful learning of concepts and principles. Novak and Gowin argue that a correct response on a multiple choice test does not necessarily indicate comprehension, since the meaning of a concept is usually acquired through sets of multiple propositions (relations or linkages between concepts) in which the concept is embedded. Furthermore, an incorrect response on an objective examination does not reveal the source or reasons for the student's wrong response, thereby making corrective measures difficult. Determining whether or not a student comprehends the meaning of a concept or proposition requires information about the way in which the concept or proposition is related to relevant concepts in the student's existing conceptual framework or cognitive structure (Ausubel, 1968; Driver and Easley, 1978; Novak and Gowin, 1984).

In order to assess the nature and cause of students' idiosyn-

cratic concept meanings and misconceptions in a given subject area, some educational researchers are employing clinical interview and concept mapping techniques as substitutes for other assessment tools (Novak, 1981; Novak and Gowin, 1984; Novik and Nussbaum, 1978; Nussbaum and Novak, 1976). These strategies have been used to reveal the relevant concepts and the number and types of conceptual linkages a student brings to a learning task. As post-instructional assessment tools, interviews and/or concept maps can be used as indicators of conceptual change, including (1) acquisition of new concepts and their integration with existing ones (2) change in the number and types of conceptual linkages (3) change in the degree of differentiation of concepts, and (4) change in pre-instructional misconceptions.

The research presented in this paper assesses college freshmen's knowledge in molecular genetics, before and after a laboratory exercise in molecular genetics, based on results from pre- and post-lab clinical interviews and multiple choice tests. The specific questions addressed by this research are:

(1) What are college freshmen's misconceptions and missing concepts in molecular genetics before and after laboratory instruction, as revealed by pre- and post-lab interviews and interview tasks?

(2) How does student comprehension and knowledge of major concepts and principles in molecular genetics change as a result of laboratory instruction, as revealed by pre- and post-lab interviews and performance on interview tasks?

(3) How do students' scores on a multiple choice test compare with their interview scores, both before and after laboratory instruction in molecular genetics?

(4) What kinds of discrepancies exist between student knowledge of molecular genetics expressed on a multiple choice test versus interviews, both before and after laboratory instruction in molecular genetics?

In this research, molecular genetics was chosen primarily as the vehicle to answer the basic questions relating to knowledge assessment by interviews versus multiple choice test items. The Central Dogma of molecular genetics, which involves DNA structure and replication, Transcription, and Translation, forms a network of conceptual relationships, such that the meaning of any particular concept, prin-

ciple or process cannot be easily understood in isolation from the rest. This paper assumes that the reader is already familiar with some of the principles and processes which comprise molecular genetics.

Methods

A. Research Subjects

The sample for this study consisted of seven student volunteers from an introductory biology course at the University of Maine. All of the participants were college freshmen who had taken a high school biology course within the past two to three years. Their majors included forestry, liberal arts, biology, pre-med, and elementary and secondary education.

B. Procedures and Materials

Experimental procedures included the following events and timeline:

> Mini-lecture on molecular genetics---10-15days---Pre-laboratory test on molecular genetics---2-5 days---Pre-laboratory interview on molecular genetics---12-14 days---Laboratory exercise on molecular genetics---7-10 days---Post-laboratory test and post-laboratory interview on molecular genetics

The lecture, which was a regularly-scheduled component of the introductory biology course, consisted of a 20-minute expository format stressing major concepts in molecular genetics. These included DNA structure and replication, the nature and function of the genetic code, the basic structure of messanger and transfer RNA, and the processes of transcription and translation and their roles in protein/enzyme synthesis. The lecture concluded with a brief summary of the relationship between DNA (genotype), protein synthesis, and phenotype.

The pre-lab test on molecular genetics was given to research participants 10-15 days after the lecture, and consisted of 16 questions, mostly multiple choice (Appendix 1). Participants were not informed of the specific subject matter under investigation prior to the pre-test and pre-interview.

The interviews were modified clinical interviews (Novak and Gowin, 1984) of 25-35 minute duration. Interview props were a model of a DNA molecule and a DNA Puzzle Kit (Carolina Biological Supply Company). Each interview started by asking students if they recognized the DNA model, after which the remainder of the interview was structured entirely around various tasks involving the DNA

Puzzle Kit. Subsequently, the laboratory exercise on molecular genetics was centered entirely around the use of the kit (Appendix 2). Since the DNA Puzzle Kit was the focus both of the interviews and the laboratory exercise, it is described briefly. It consists of cardboard cut-outs of various shapes and colors, representing the basic chemical components of DNA and messanger RNA (deoxyribose sugar, ribose sugar, phosphates, nitrogenous bases - adenine, thymine, guanine, cytosine, uracil). The structural formula of each chemical unit is printed on the corresponding cut-out. Each nitrogenous base unit is labeled either A, T, C, or G, representing the first letter of the nitrogenous base represented by the cut-out. The cut-outs fit together as in a picture puzzle, so that only the appropriate chemical units can be joined to eachother. This permits assembly of models of DNA and messanger RNA (mRNA) and, by various manipulations, illustrates the processes of DNA replication and RNA transcription.To illustrate translation, the kit includes large cut-outs of transfer RNA molecules (tRNA), smaller cut-outs of specific amino acids which can be joined only with their corresponding tRNA units, and a ribosome template. The tRNA units are labeled TRNA and the amino acid units are labeled with the name of a amino acid. One end of each tRNA unit has a cut-out pattern which allows the unit to be joined only to a specific (complimentary) nitrogenous base triplet (codon) of a pre-constructed mRNA strand. The ribosome template consists of a large piece of heavy paper with a schematic drawing of a ribosome, including 40S and 60S subunits (with P and A sites indicated). This arrangement allows a preconstructed mRNA strand to be placed on the 40S subunit. A tRNA cut-out, together with its amino acid, is then placed on the P site to determine if its terminal cut-out pattern can be joined to the cut-out pattern of the nitrogenous base triplet of the mRNA strand located above the P site. The same procedure is then followed for the A site. The P site amino acid is detached from its tRNA unit and connected to the A site amino acid. The P site tRNA unit is removed, and the mRNA strand is moved so that the A site tRNA unit, now with a chain of two amino acids, occupies the P site. This frees the A site for another tRNA unit with its attached amino acid. The two amino acids on the P site tRNA are detached and joined to the amino acid of the tRNA on the A site. In this way, a short polypeptide is built, and the relationship between

mRNA and tRNA in the process of protein synthesis is illustrated.

Prior to each interview, three stations were set up, each with a different component of the DNA Puzzle Kit, and stressing different concepts and tasks (Table 1). Critical concepts brought up during questioning at one station were often probed further and in different contexts at succeeding stations to identify unstable responses.

Interview questions were based on five major organizing principles, including DNA structure and location, DNA Replication, Transcription, Translation, and DNA-RNA-Phenotype relationship (Table 2, I-V). Each of these organizing principles was subdivided into a number of subsidiary principles which formed the focus of interview questions (Table 2, 1-20). Additional details were provided by consulting a pre-constructed interview concept map (Figure 1). All concepts and principles covered in the interviews came from the introductory lecture and the student laboratory hand-out on molecular genetics (Appendix 2).

Questions asked during the interview had a sequence only insofar that they corresponded to the student's progression from one interview station to the next. If a student's response to a question made it feasible to follow up with a question normally asked during a later part of the interview, that question was asked in order to maintain the flow of the interview. The question was then asked again at a later time, usually in a different context. Consequently, the interviews were semi-flexible, being guided by a general plan.

The laboratory exercise on molecular genetics occurred about two weeks after the pre-test and pre-interview. During the two-hour laboratory session, which was a regular component of the introductory biology course, students worked in pairs with the DNA Puzzle Kit. Pre-tested-pre-interviewed students were paired up with students not involved in the research project.

Post-lab interviews were of the same format as the pre-lab interviews, and the post-lab test was identical to the pre-lab test. The post-lab test was administered immediately after each post-lab interview. Students were asked not to review for the post-test and interview.

C. Analyses

Transcripts of taped interviews (see Appendix 3 for examples of interview transcripts) were analyzed to determine students' miscon-

Table 1. Props, Concept categories, and tasks associated with various pre- and post-laboratory interview stations.

Station #	Props	Concept Categories Probed	Tasks
1	1) picture of DNA model 2) pre-assembled single DNA strand 3) Various free DNA nucleotide units scattered randomly next to assembled strand	1) DNA structure, function 2) Gentic code and codons 3) DNA replication 4) Relationship between DNA and RNA 5) Significance of nitrogenous base sequence; protein synthesis	1) construction of a complete DNA molecule from the pre-assembled strand, using available free nucleotides 2) DNA replication
2	1) pre-assembled single DNA strand (9 nucleotides) 2) Various free RNA nucleotides scattered randomly next to assembled DNA strand	1) mRNA structure, function; compared to DNA 2) mRNA synthesis-transcription 3) transfer of DNA code to mRNA; base sequence 4) role of tRNA; relation to m RNA; protein synthesis 5) general probe into process of translation	3) transcription; construction of mRNA strand using, a. pre-assembled single DNA strand as a template, and, b. available free mRNA nucleotides 4) separation of mRNA strand from DNA template strand
3	1) mRNA strand from station 2 2) tRNA units with attached amino acids 3) ribosome template	1) translation; protein synthesis 2) relationship between DNA structure (genetic code, genotype), protein/enzyme synthesis, and phenotype	5) translation; transfer of mRNA to ribosome template; hook-up of tRNA to mRNA base triplets; joining of amino acids into short polypeptide chain

Table 2. Major organizing principles and subsidiary principles used as questioning guides during pre- and post-lab interviews on molecular genetics.

Major Principle or Process

I. DNA Structure, Location

1. DNA is part of chromosomes and genes and is located in the cell nucleus.

2. DNA is a double-strand (alpha helix) molecule consisting of basic structural units called nucleotides, which consist of phosphate, deoxyribose sugar and a nitrogenous base.

3. The nitrogenous bases are adenine, thymine, guanine and cytosine, arranged in complimentary base pairs (A-T, C-G) which connect the DNA strands by weak hydrogen bonds.

4. The bases in a DNA strand have a sequence/order which represents genetic information (=genetic code) for the assembly of amino acids and proteins.

5. The DNA code is a sequence of codons, which are groups of 3 (triplet) nitrogenous bases that code for an amino acid.

II. DNA Replication

6. The DNA double strand can separate into two single strands by the breakage of weak hydrogen bonds between the bases.

7. The single strands each have a base sequence which acts as a template/model for assembly of the missing strand from free, available nucleotides; there is complimentary base pairing between bases of template strand and bases of free nucleotides.

8. The result of replication is two double-stranded DNA molecules, identical to eachother and to the original double-stranded molecule which underwent replication.

III. Transcription

9. A single DNA strand in the nucleus can assemble a RNA strand by base pairing between DNA and RNA bases; RNA bases are part of free, available RNA nucleotides in the cell nucleus.

10. The sequence of RNA bases in an assembled RNA strand is determined by the base sequence of the model DNA strand, and represents the genetic code of DNA, transferred to RNA.

11. RNA is a single strand, either messanger or transfer RNA, consisting of RNA nucleotides, which are composed of phosphate, ribose sugar, and a nitrogenous base--either adenine, guanine, cytosine or uracil (instead of thymine).

12. In the assembly of RNA from DNA, base pairing is A-U, T-A, C-G, G-C (DNA-RNA).

13. The assembled RNA strand separates from the DNA strand, leaves the nucleus, and goes to the ribosomes in the cytoplasm.

Table 2. Continued.

IV. Translation

14. Translation occurs at the ribosomes, involves mRNA and tRNA, and results in assembly of amino acids into proteins.

15. mRNA is a single strand with many exposed nitrogenous bases; it has a base sequence which compliments the base sequence of the DNA strand from which it was made, and which represents a genetic code of numerous RNA codons---a combination of 3 mRNA bases/nucleotides.

16. Each mRNA codon codes for an amino acid and the sequence of codons in the mRNA strand will determine the sequence in which amino acids will be linked together to form a specific protein.

17. tRNA is a single strand, but is looped, thereby exposing only one base triplet (codon/anti-codon) and one amino acid binding site; the binding site bonds to a specific amino acid, based on the exposed codon/anti-codon unit and general structure of the tRNA strand.

18. tRNA picks up amino acids (one per tRNA molecule) in the cell cytoplasm and goes to a ribosome, where its anti-codon hooks up with a complimentary mRNA codon; tRNA releases its amino acid to join up with amino acids brought in by other tRNA molecules, thereby forming a specific protein, determined by the sequence of mRNA codons.

V. DNA—RNA—Phenotype

19. The genetic code in DNA of an organism is transferred to RNA (mRNA and tRNA) and is indirectly involved in the synthesis of specific proteins, as dictated by the organism's unique DNA code (sequence of bases/codons).

20. The specific set of proteins made by an organism includes structural and functional proteins (enzymes), which determine the organism's unique phenotype (appearance and functioning) by regulating the organism's biochemical, structural and developemtal processes; differences in phenotype are related to differences in proteins caused by differences in DNA code of organisms.

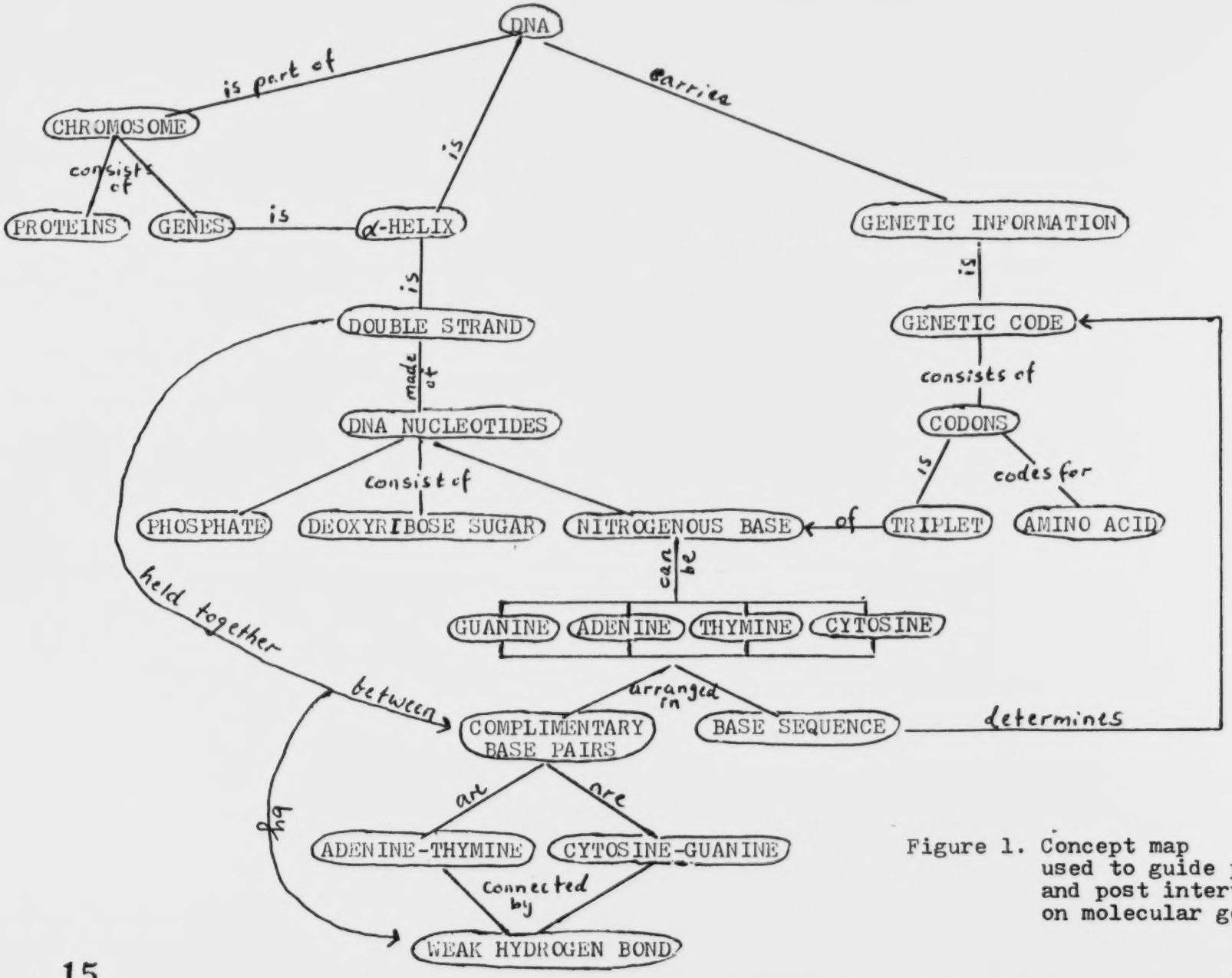


Figure 1. Concept map used to guide pre- and post interviews on molecular genetics.

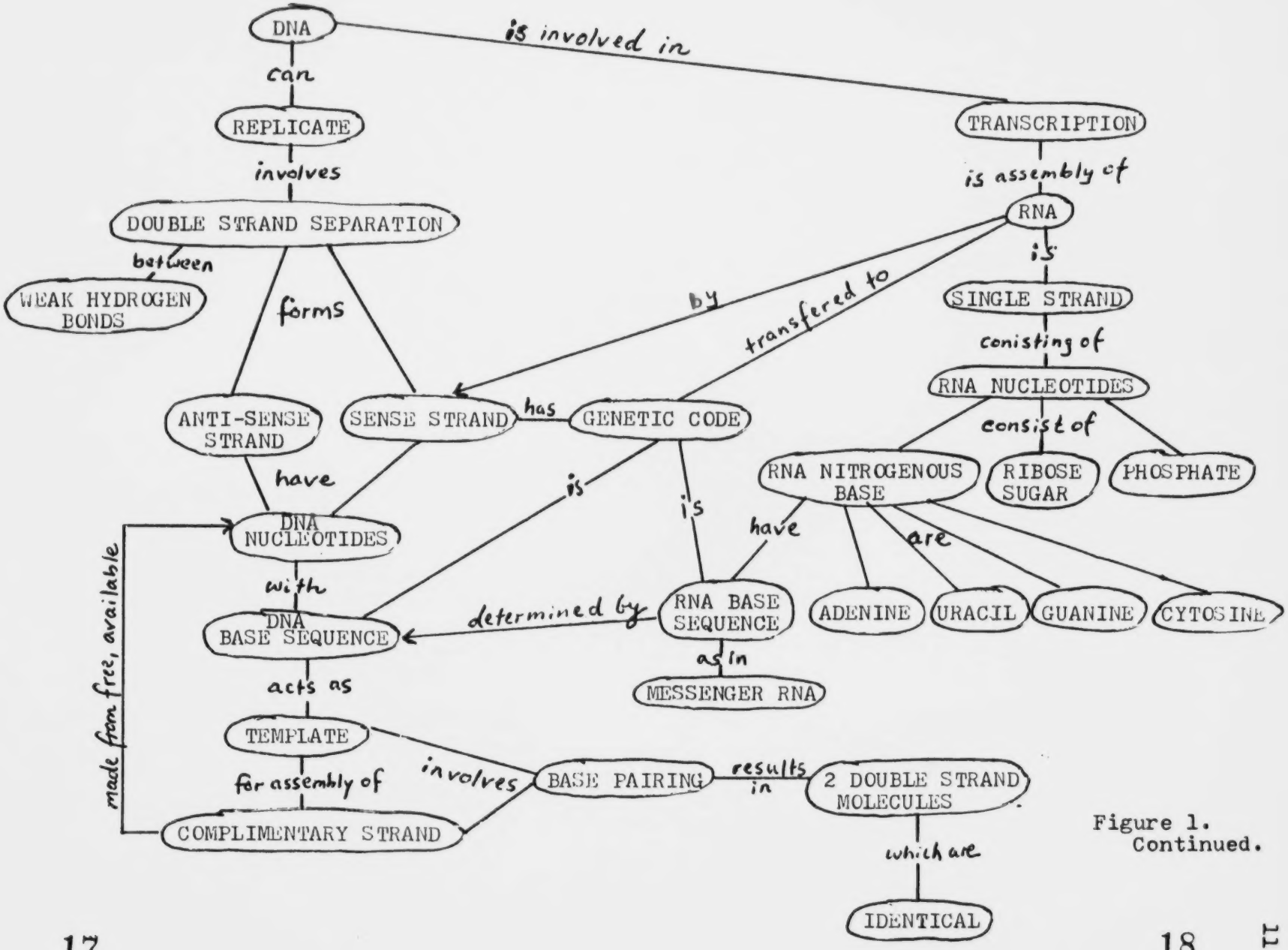


Figure 1.
Continued.

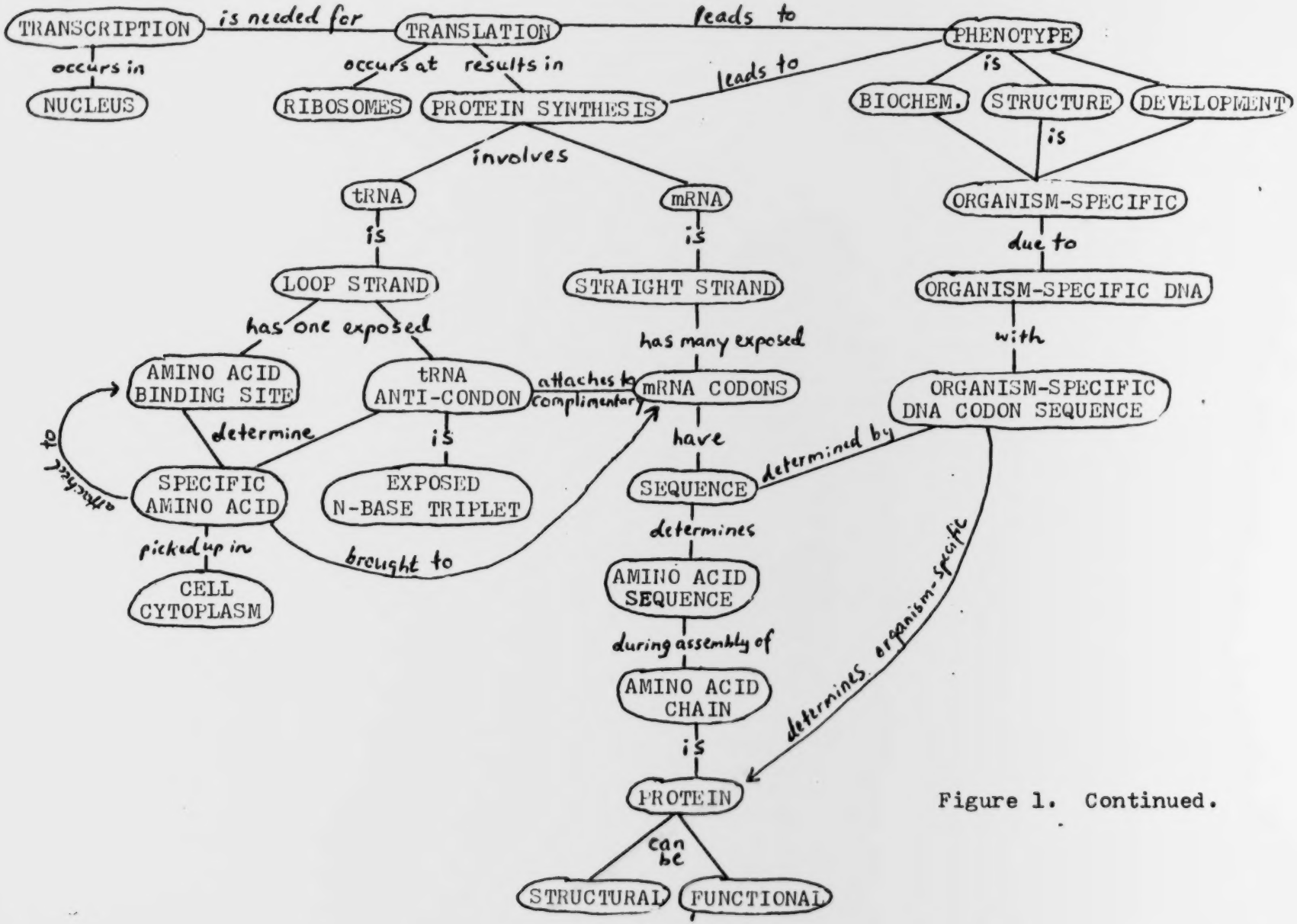


Figure 1. Continued.

ceptions and missing concepts or principles before and after laboratory instruction. The percentage of students lacking a given concept, proposition or principle , or holding a certain misconception, was calcalculated. Total and mean number of missing concepts and misconceptions per student were determined from pre- and post-laboratory interviews. Concept maps were constructed from the transcripts of two student interviews to show changes in concept differentiation, concept-propositional linkages, and misconceptions as a result of laboratory instruction.

During the interviews, students were scored on task performance, using the scoring scale and criteria in table 3. The table also shows the scoring scale and criteria used to evaluate each student's pre- and post-instructional knowledge of each subsidiary principle (Table 2, 1-20). A student who lacked all of the necessary concepts contained within a certain principle, or who had a complete misconception regarding the meaning of a principle or proposition (all concept linkages incorrect), was given a score of "0". Although a complete misconception and a completely missing principle/proposition are not the same and have different instructional implications, they may be considered quantitatively identical for scoring purposes, since both indicate that the student lacks proper understanding of the principle. Also, when a principle consists of a number of concepts and concept linkages, a student's comprehension of the principle may have minor misconceptions embedded within it. These situations were considered and incorporated into the scoring criteria as shown for scores of "1" and "2" (mix of missing, incorrect, correct, and vague concept linkages), in table 3.

Each student was scored on each subsidiary principle (pre- and post laboratory instruction). The scores for the subsidiary principles within each major organizing principle category (see table 2, I-V) were averaged and converted to a percentage (4=100%) to show pre-post percentage scores for each major organizing category, for each student. A total average score, based on all subsidiary principles, was calculated for each student and converted to a percentage to show total percent score (pre,post) and total percent score change after laboratory instruction. The scores of all students were averaged for each subsidiary principle to show mean raw scores, mean percentage scores and mean percent score changes for each subsidiary principle, major organizing category, and all principles combined (overall grand mean). Identical procedures were used to analyze and summarize performance on interview

Table 3. Interview scoring scale and criteria for subsidiary principles and interview tasks.

Scoring of Subsidiary Principles	Scoring of Tasks
0 = No concepts/Complete Misconception (all concept linkages incorrect)	0 = Incapable of performing or explaining task
1 = Some concepts of principle present (less than 50%) but with a mix of missing, incorrect, and vague concept linkages	1 = Task partially/completely performed, but with elements of trial-and error, uncertainties or erroneous reasoning or explanations
2 = Some to most concepts of principle present (50-75%) but with a mix of missing, incorrect, correct and vague concept linkages	2 = Task performed correctly, with correct reasoning and explanations
3 = Most to all concepts of principle present (75-100%) but with some vague or uncertain concept linkages	
4 = All concepts and correct concept linkages present	

tasks.

Multiple choice test items were grouped according to the major organizing principles which structured the interviews (see Appendix 2 for grouping). Questions relating to organizing principle V (see Table 2) were not included on the multiple choice test and only two test questions involved organizing principle II. Consequently, subsequent comparisons between student performance during interviews and on the multiple choice test did not include any comparisons between major organizing principles II and V. Each student's pre- and post instruction test scores on organizing principles I, III, and IV were converted to percentage scores and compared with scores derived from interviews. Also, each student's total percent test score (pre, post) for the three organizing principles combined, were compared with their interview scores on these principles. Mean pre- and post-laboratory test scores were calculated for each of the three organizing principle categories and for the combined categories (grand mean). Mean test scores and mean score changes (pre- to post) were compared with mean scores and score changes derived from interviews.

Comparison of students' interview and test performances on specific items, concepts, and principles revealed some major discrepancies between knowledge expressed during interviews and on the test. The discrepancy rating categories and their explanations are shown in table 4. For each student, pre-test-pre-interview and post-test-post-interview discrepancies were organized into discrepancy rating categories and were counted. This revealed which types of discrepancies were predominant before laboratory instruction, and how the discrepancies changed after instruction. A similar discrepancy analysis was made for each major principle category to determine which category showed the most discrepancies, the predominant types of discrepancies, and how these changed for each major organizing principle category after laboratory instruction.

Table 4. Multiple choice test — Interview discrepancy ratings and explanations.

Discrepancy Rating	Explanation
0 +	Student answered test item incorrectly but understood principle during interview.
0 +/-	Student answered test item incorrectly but had a partial understanding of the principle during interview.
1 -	Student answered test item correctly but had little to no understanding of principle during interview.
1 +/-	Student answered test item correctly but had only a partial understanding of principle during interview, with some missing concepts and/or some incorrect or vague concept linkages.

Results

Tables 5 and 6 show that students were missing numerous concepts and propositions and had a variety of misconceptions during the pre-laboratory interview, despite their exposure to the introductory lecture in molecular genetics. The mean number of misconceptions was lower than the mean number of missing concepts/propositions (5.6 versus 7.6), although the total number of misconceptions was more than twice the number of missing concepts/propositions (25 vs. 11). This is because misconceptions were much more idiosyncratic than missing concepts. A comparison of the tables shows that the proportion of students lacking a certain concept/proposition was generally higher than the proportion of students having a certain misconception. A similar pattern was observed for the post-lab interviews (tables 7 and 8), although the number of missing concepts and misconceptions were lower. The mean number of missing concepts/propositions declined from 7.6 to 2.0, and the mean number of misconceptions dropped from 5.6 to 1.6.

Table 5 shows that concepts and subsidiary principles related to major organizing principle V (DNA-RNA-Protein synthesis-Phenotype) were missing in all students during the pre-lab interview. Several students knew some of these concepts, but none had a clear understanding of all relevant reationships in this category. During the post-lab interview, one student was still missing some of these concepts (table 7), but there were no misconceptions regarding the concepts and propositions in category V. The concepts and propositions (and subsidiary principles) in category V are critical for a comprehension of the Central Dogma of molecular genetics, since they explain and synthesize the functions and ultimate purpose of DNA. The results of pre-lab interviews showed that students knew some of the isolated concepts and processes in molecular genetics, but generally did not clearly understand their relationship and overall significance.

Major concepts and propositions which were still missing in some students despite laboratory instruction included the type and strength of bonds connecting the DNA strands, and structural differences between messanger and transfer RNA(table 7). Post-lab misconceptions covered a wide range and were highly idiosyncratic (table 8). Most of them were confined to student #2.

Table 5. Missing concepts and principles during pre-laboratory interviews, arranged according to major organizing principles (I-V).

Missing Concepts/Principles	Student 1	2	3	4	5	%
I.						
1. Nucleotides are the basic structural units of DNA (phosphate, sugar, nitrogenous base)	x	x	x	x	x	100
2. The genetic code is a series of codons/base triplets		x				20
3. Codon (concept label)	x	x		x		60
4. A codon can be any arrangement of 3 bases/nucleotides		x	x			40
5. Weak hydrogen bonds connect base pairs of DNA strands		x		x	x	60
II.						
No missing concepts (major)						
III.						
6. Nucleotides are basic structural units of mRNA and tRNA	x	x	x	x	x	100
7. The DNA code is transferred to RNA by assembly of RNA strand from a DNA strand		x				20
IV.						
8. Concepts related to structure of tRNA	x	x	x	x	x	100
9. An amino acid is bonded to each tRNA molecule	x	x		x		60
10. Conceptual details of translation process - mRNA, tRNA relationships in protein synthesis	x	x	x	x	x	100
V.						
11. DNA-RNA-Protein synthesis-Phenotype relationship	x	x	x	x	x	100
Total Missing/Student:	7	11	6	8	6	
Mean ± S.D: 7.6 ± 2.1						

Table 6. Student misconceptions during pre-laboratory interviews, arranged according to major organizing principles (I-V).

Misconceptions	Student 1	2	3	4	5	%
I.						
1. DNA has amino acids in it	x		x		x	60
2. DNA is made of proteins		x				20
3. DNA has glucose sugar in it		x				20
4. Adenine, thymine, etc. are different genes	x					20
5. Adenine, thymine, etc. are different amino acids				x		20
6. The basic unit of DNA is amino acids					x	20
7. DNA strands are held together by proteins and charges		x				20
8. The genetic code consists of amino acids and proteins		x				20
9. The DNA code is determined by bonds and nucleotides		x				20
10. The hydrogen bonds connecting bases of DNA are strong				x	x	40
11. Codons are patterns of base pairs			x			20
12. Codons must have a definite sequence			x			20
II.						
No major misconceptions						
III.						
13. RNA is put together in nucleus and cytoplasm				x		20
14. RNA occurs only at the ribosomes		x				20
15. RNA is a double strand with uracil instead of thymine (DNA changes to RNA)		x				20
16. tRNA is made from messanger RNA				x		20
IV.						
17. The "ribo" in RNA stands for ribosome		x				20
18. Proteins and amino acids are changed into RNA at the ribosomes		x				20
19. Ribosomes store energy and proteins		x				20
20. Proteins are synthesized at ribosomes to get energy		x				20
21. mRNA stays on DNA and reads it				x		20
22. Amino acids are attached to mRNA				x		20

Table 6. Continued.

Misconceptions	Student 1	2	3	4	5	%
23. m RNA reads DNA and this causes amino acids on mRNA to hook together to form proteins				x		20.
24. Ribosomes are attached to mRNA and help mRNA to read DNA				x		20
25. tRNA gets mRNA (and its amino acid) to DNA, so mRNA can read the DNA				x		20
Total Misconceptions/Student:	2	11	3	9	3	
Mean ± S.D.: 5.6 ± 4.1						

Table 7. Missing concepts and principles during post-laboratory interviews, arranged according to major organizing principles (I-V).

	Student							
Missing Concepts/Principles	1	2	3	4	5	6	7	%
I.								
1. Nucleotide (concept label)				x		x	x	43
2. Codon (concept label)				x				14
3. Hydrogen bonds connect DNA strands		x					x	29
4. Bonds connecting DNA strands are weak, to facilitate strand separation		x		x	x	x		57
II.								
No missing concepts								
III.								
No missing concepts								
IV.								
5. Concepts related to structural differences between mRNA and tRNA		x			x			29
6. Concepts related to details of translation process; relationship between mRNA, tRNA, ribosomes and protein synthesis		x						14
V.								
7. Elements of DNA-RNA-Protein synthesis-Phenotype relationship		x						14
Total Missing/Student:	0	5	0	3	2	2	2	
Mean ± S.D.: 2.0 ± 1.7								

Table 8. Student misconceptions during post-laboratory interviews, arranged according to major organizing principles (I-V).

Misconceptions	1	2	3	4	5	6	7	%
I.								
1. Adenine, thymine, etc. are amino acids							x	14
2. Strong hydrogen bonds are needed between base pairs to hold DNA strands together				x				14
3. Bonds connecting DNA strands are strong polypeptide bonds		x						14
4. A codon is a pair of nitrogenous base triplets	x							14
5. A codon codes for a protein or amino acid		x						14
6. A codon "creates" a specific amino acid		x						14
II.								
No misconceptions								
III.								
7. mRNA is made in ribosomes/nucleus		x						14
IV.								
8. mRNA comes to nucleus to read DNA		x						14
9. Glycine and alanine are chemicals made by amino acids		x						14
10. tRNA creates amino acids		x						14
11. mRNA gives message to tRNA to create a amino acid		x						14
V.								
No major misconceptions								
Total Misconceptions/Std.:	1	8	0	1	0	0	1	
Mean +/- S.D.: 1.6 +/- 2.9								

Sudent #2 was the only student who was still missing certain key concepts and concept relationships in major category V, after laboratory instruction. This might explain some of the difficulties student #2 had with some of the other concepts and concept relationships in molecular genetics. Although the number of misconceptions for student #2 dropped by only 3 (from 11 to 8) between the pre- and post-lab interviews, the post-lab misconceptions were less severe. They involved primarily certain specifics, and did not substantially affect comprehension of more critical and inclusive concept and principle relationships. Figures 2 and 3 are pre- and post-lab concept maps constructed from student #2's interview transcripts. The post-lab concept maps show increased concept differentiation and a greater number of correct concept linkages and propositions.

Student #4 was an interesting example of someone who knew many of the concept lables during the pre-lab interview, but did not know their relationship or what they meant. He commented: "I know all the terms but don't know how they're connected". As did most of the other students, he had considerable difficulty understanding the translation process. He knew many of the relevant concept labels, but his attempts to explain their relationship and meaning resulted in a number of serious and highly unique misconceptions (table 6; misconceptions 21-25). These are diagrammed in figure 4A. The student knew that the result of translation is protein synthesis, but the intermediary propositions he proposed were mainly invalid. The most serious misconception was the idea that the assmebly of mRNA by DNA, and protein synthesis, occur simultaneously within the nucleus. This made sense to the student because he believed mRNA (rather than tRNA) to carry amino acids. Thus, during the assembly of mRNA units into a mRNA strand by a DNA strand template, protein synthesis is concurrently accomplished by the bonding of the amino acids carried by mRNA units. The student accounted for tRNA by suggesting that it carries the mRNA (presumably mRNA units and their amino acids) from the cytoplasm to the DNA in the nucleus. He regarded ribosomes as some nebulous structures attached to mRNA units, helping them to read DNA, rather than as discrete cytoplasmic organelles at which translation and protein synthesis take place. These explanations represent a rational attempt to unite a group of vague, undifferentiated concept labels into meaningful propositions. The student was forced to "create" conceptual linkages

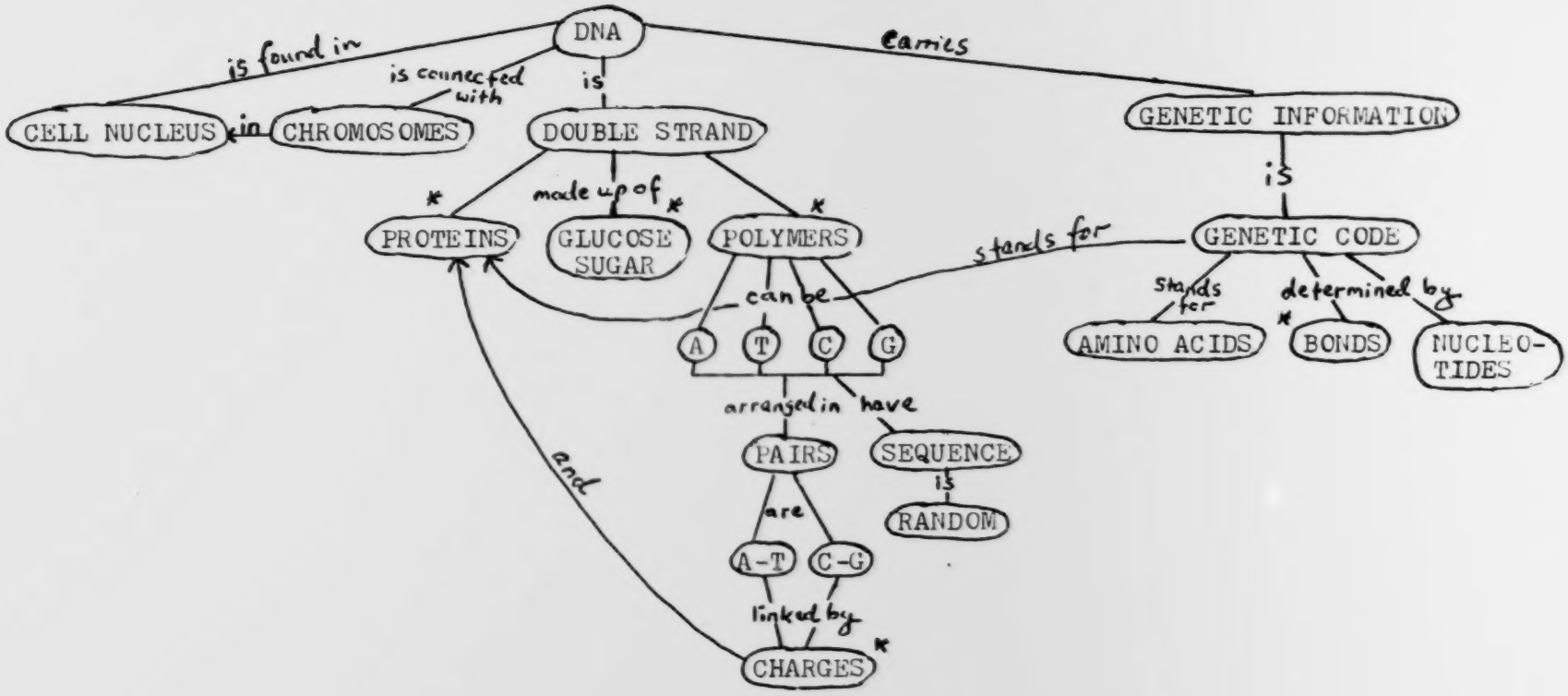


Figure 2. Pre-lab interview concepts map constructed from interview transcript of student #2. Asterisks denote incorrect concept or concept linkage.

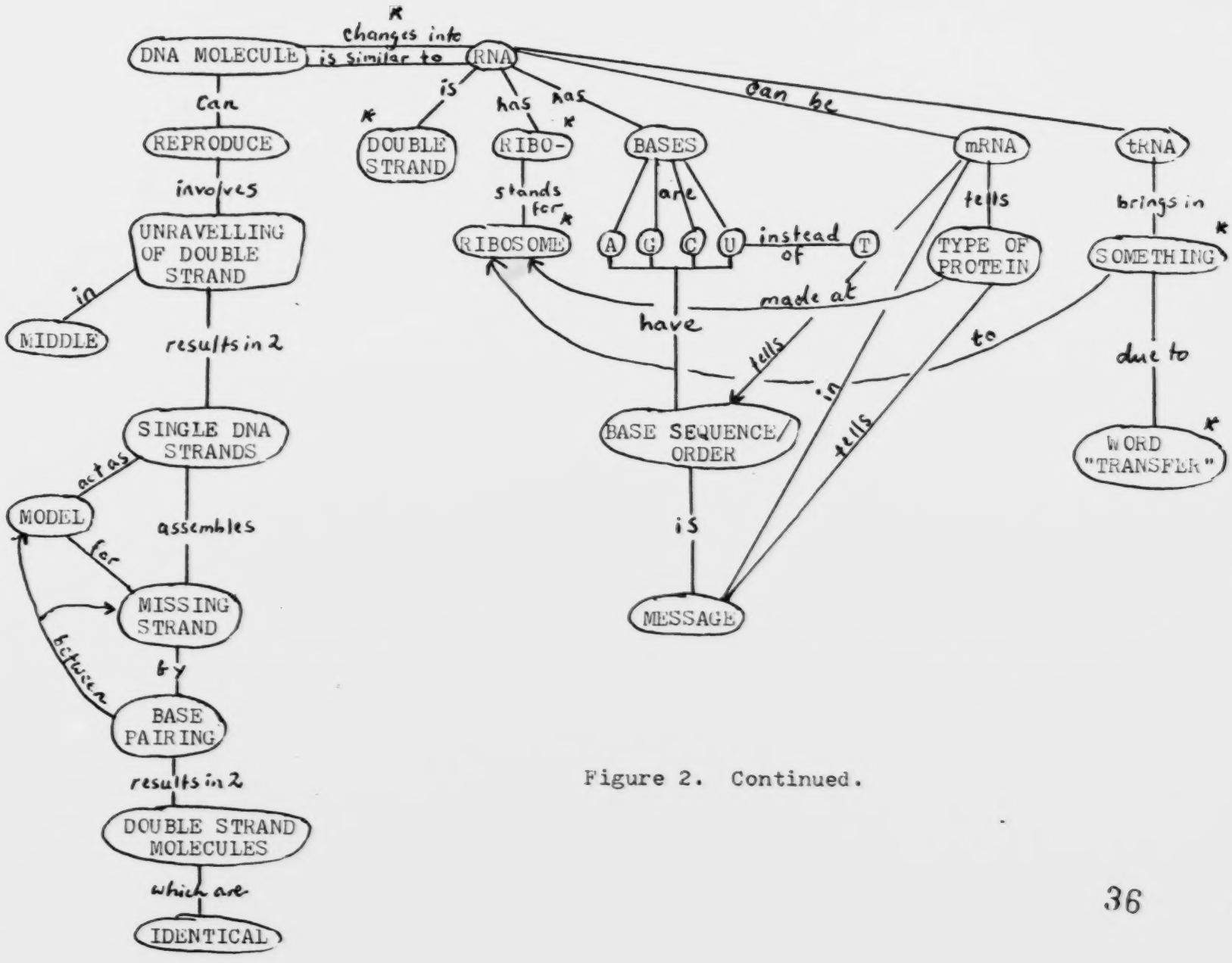


Figure 2. Continued.

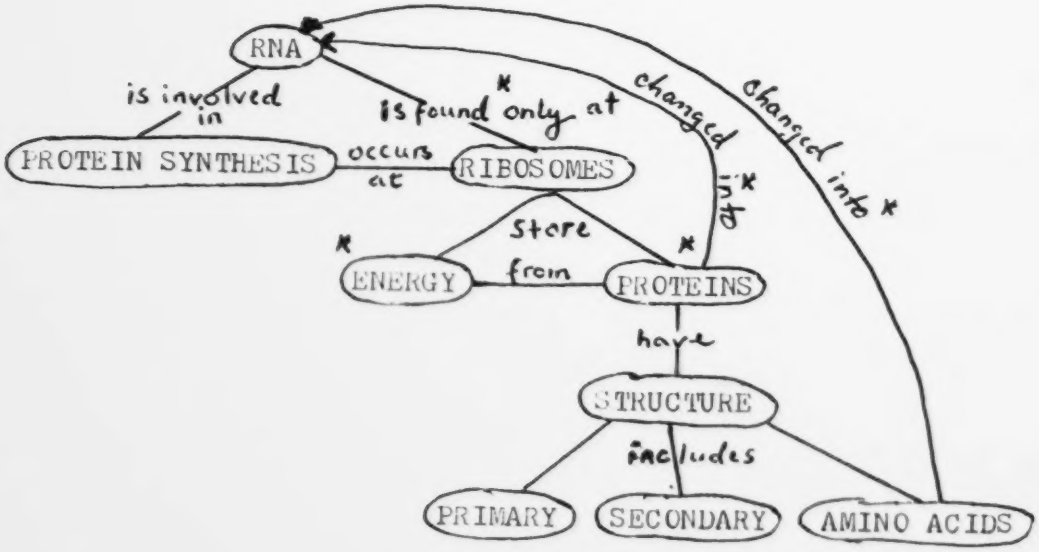


Figure 2. Continued.

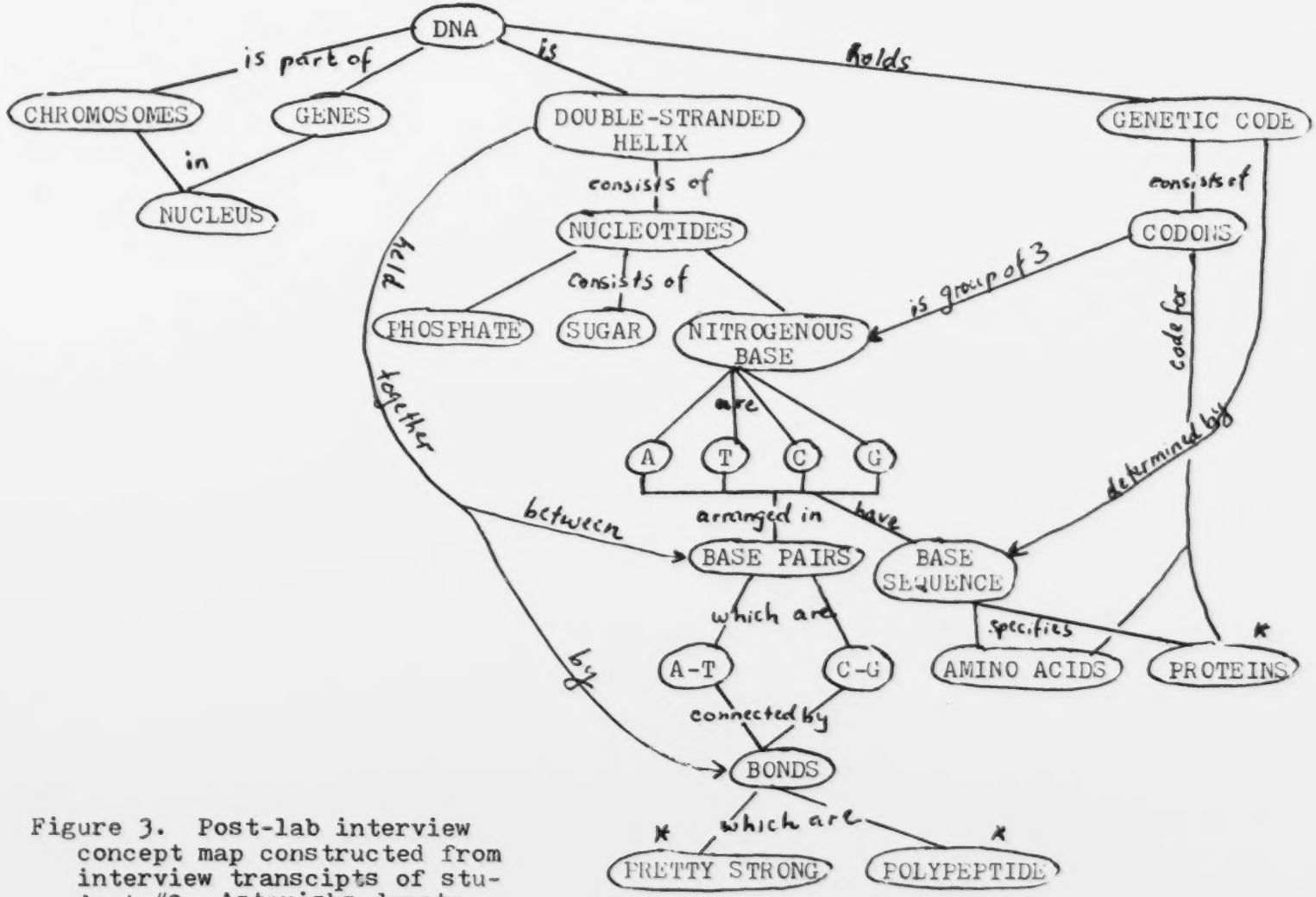


Figure 3. Post-lab interview concept map constructed from interview transcipts of student #2. Asterisks denote incorrect concept or concept linkage.

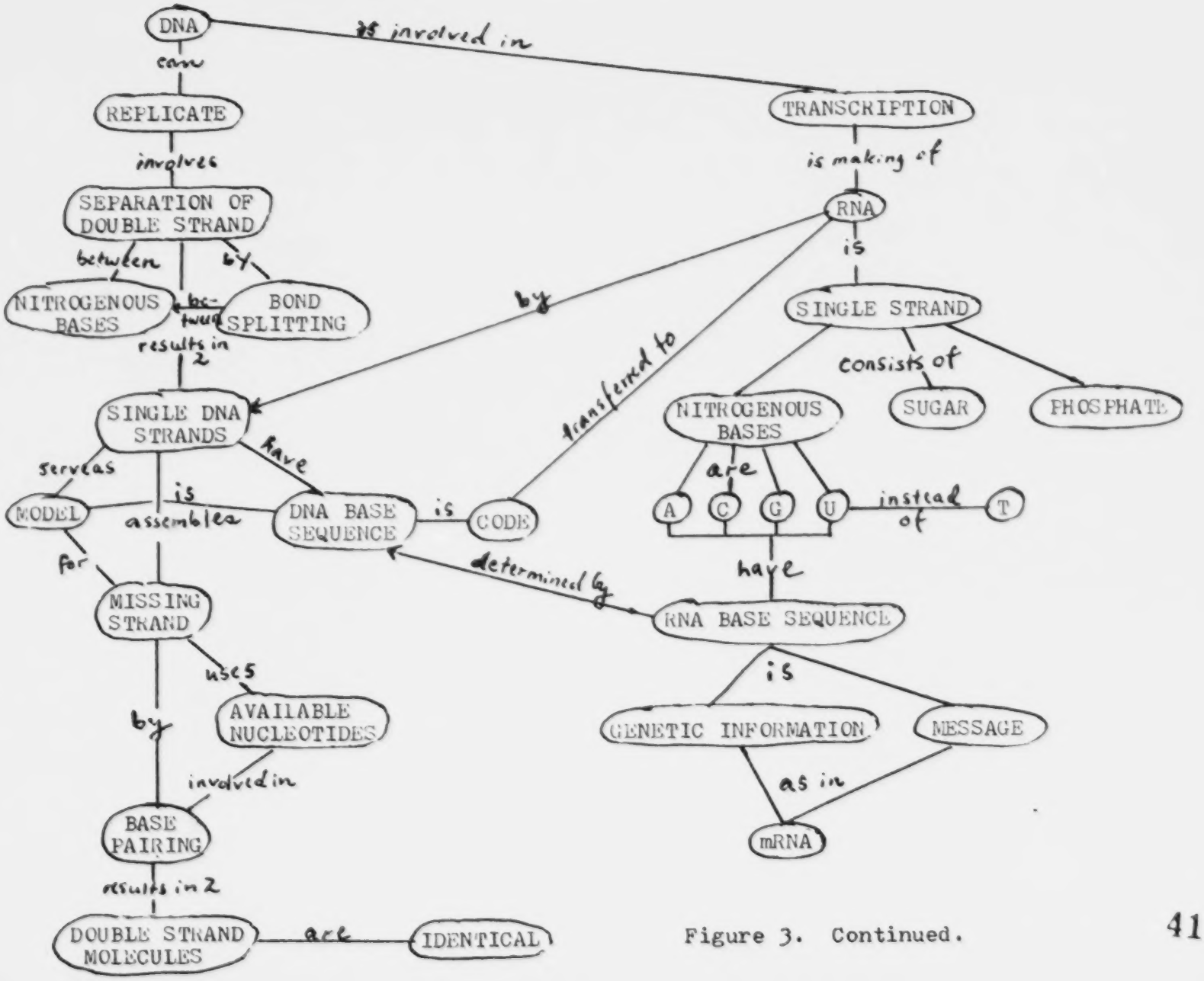


Figure 3. Continued.

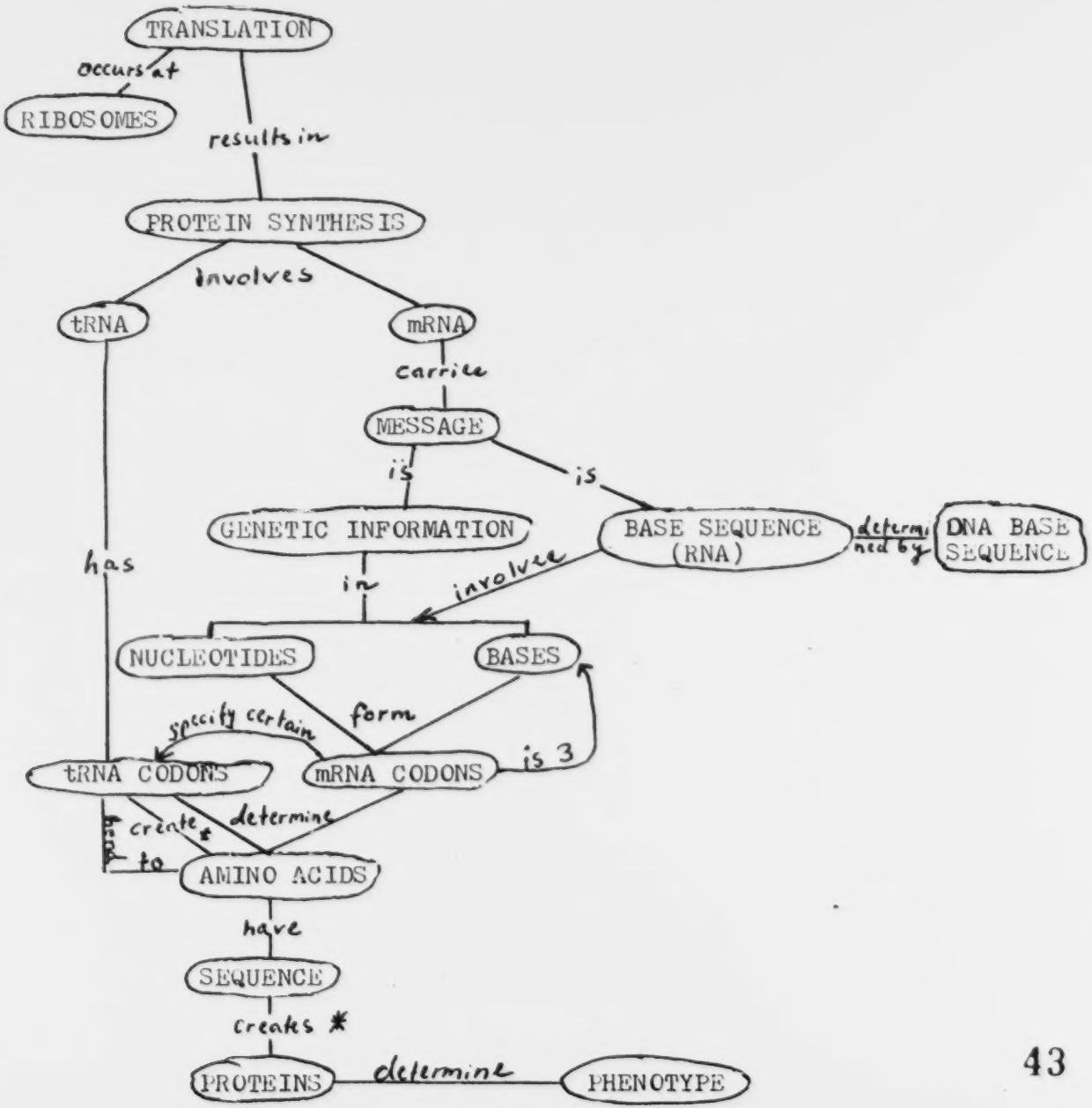
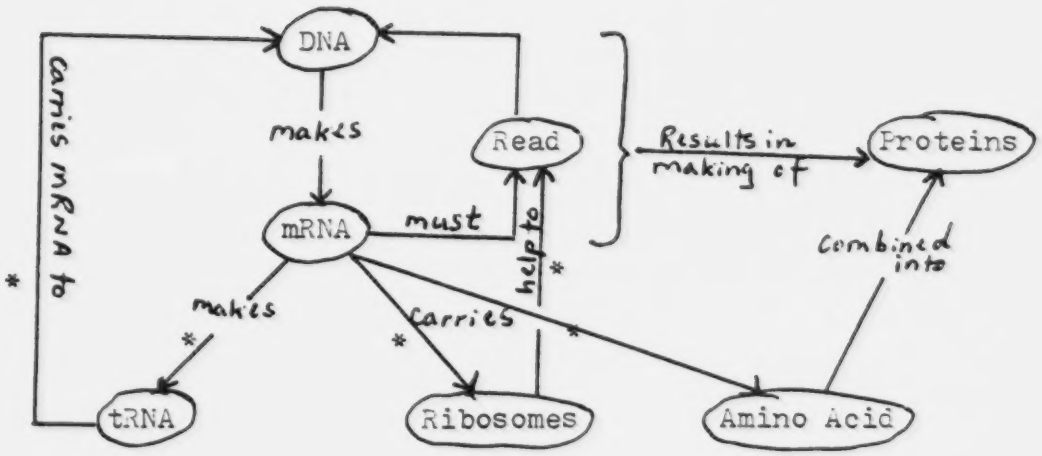


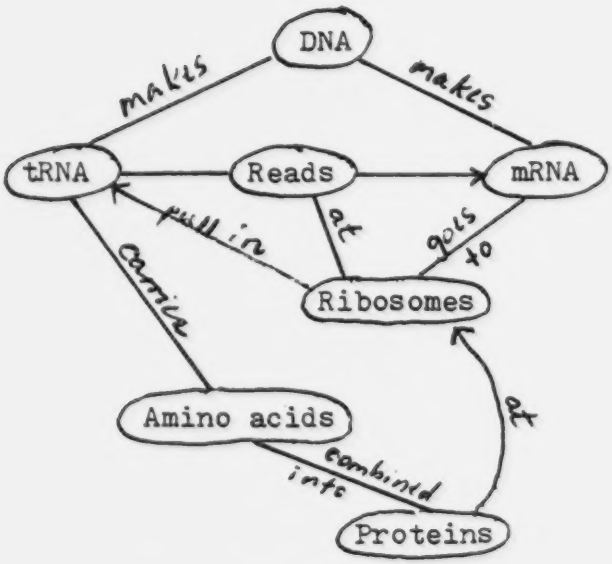
Figure 3. Continued.

Figure 4. Pre-lab (A) and post-lab (B) interview concept maps of transcription and translation processes constructed from student #4 interview transcripts. Asterisks denote incorrect concept or concept linkage.

A.



B.



that could be supported by the limited differentiation of available concepts. This resulted in a set of erroneous propositions which were subsequently replaced by correct conceptual linkages following the laboratory exercise in molecular genetics (figure 4B).

Table 9 presents statistics on student performance on each subsidiary principle (pre- and post lab interviews), percentage scores for each major organizing category, and total percentage score and pre-post score change for all principles combined. All students showed significant improvement following the laboratory exercise. It is significant that, although student #2 had the lowest pre- and post-lab interview scores (29 and 76%, respectively), he showed the greatest improvement, with a total score change of 47%. Table 9 also provides a key permitting interpretation of percentage scores in terms of the scoring scale criteria for subsidiary principles.

Table 10 shows mean pre- and post-lab interview scores for each subsidiary principle, each major organizing category (grand mean), and the mean percentage score change for each subsidiary principle and organizing category. Also shown are the overall grand mean pre-post scores for all principles combined, and the grand mean percentage score change. The lowest mean scores, both pre- and post-lab, were on principles 20 and 17 which related to the DNA-RNA-Phenotype linkage and the structure of transfer RNA. However, students showed the greatest increase in comprehension of these principles after laboratory instruction, with a score increase of 55-60%. A similar pattern was evident with major categories IV and V. The overall pre-lab grand mean score of 2.3 (58%), when compared to the scoring criteria at the end of table 9, indicates that, on average, students had some knowledge of concepts in molecular genetics prior to laboratory instruction, but with a mix of missing, incorrect, correct, and vague concept linkages. The post-lab grand mean interview score of 3.49 (87%) suggests that students knew most of the concepts and principles after laboratory instruction, although some concept linkages were still vague or uncertain.

Table 11 shows students' pre- and post-lab interview task performance scores, total percent score on all tasks, and total score change (%). There was a fairly good correlation between a student's total percent task score and score change, and his/her total percent score and score change on concepts and principles (see table 9). In all cases where a task was not performed correctly during the pre-lab interview, there was improvement in task performance during the post-lab in-

Table 9. Student pre- and post-lab interview scores for each subsidiary principle, percent scores (4=100%) for each major organizing category (I-V), total percent scores, and total pre- post-lab score changes (%).

PRINCIPLE	Student 1		2		3		4		5	
	Pre	Post	Pre	Post	Pre	Post	Pre	Post	Pre	Post
I.										
(1)	3	3	3	3	4	4	3	3	3	3
(2)	2	4	2	4	2	4	2	3	2	4
(3)	3	4	2	2	4	4	2	2	2	3
(4)	3	4	1	3	3	4	2	4	3	4
(5)	3	3	0	3	2	4	2	3	3	4
% Score:	70	90	40	75	75	100	55	75	65	90
II.										
(6)	4	4	2	3	4	4	3	3	3	3
(7)	3	4	3	4	4	4	3	4	4	4
(8)	3	3	2	4	3	4	3	3	3	4
% Score:	83	92	58	92	92	100	75	83	83	92
III.										
(9)	3	4	0	3	4	4	2	3	4	4
(10)	4	4	1	3	4	4	2	4	4	4
(11)	2	3	1	3	2	4	2	3	2	3
(12)	4	4	1	3	3	4	3	4	4	4
(13)	4	4	1	4	4	4	0	4	3	4
% Score:	85	95	20	80	85	100	45	90	85	95
IV.										
(14)	3	4	2	3	4	4	1	3	3	4
(15)	3	4	0	4	3	3	2	4	3	3
(16)	2	4	1	3	3	4	2	4	3	4
(17)	0	3	0	2	2	3	0	3	1	3
(18)	1	3	0	2	3	4	0	4	2	3
% Score:	30	90	15	70	75	90	25	90	60	85

Table 9. Continued.

PRINCIPLE	Student 1 Pre	1 Post	2 Pre	2 Post	3 Pre	3 Post	4 Pre	4 Post	5 Pre	5 Post
V.										
(19)	2	4	1	3	4	4	2	3	3	3
(20)	1	3	0	2	1	3	0	3	0	3
% Score:	38	88	13	63	63	88	25	75	38	75
Total % Score:	63	91	29	76	79	96	45	84	69	89
Change (%):	+28		+47		+17		+39		+20	

% Score	Score Meaning in Relation to Subsidiary Principle Scoring Scale
0	(0) No concepts/Complete Misconception
25	(1) Some concepts (less than 50%), with a mix of missing, incorrect, and vague concept linkages
50	(2) Some to most concepts (50-75%), with a mix of missing, incorrect, correct and vague concept linkages
75	(3) Most to all concepts (75-100%) but with some vague or uncertain concept linkages
100	(4) All concepts and correct concept linkages present

Table 10. Mean pre- and post-lab interview scores and score changes for each subsidiary principle, each major organizing category (grand mean), and for all principles combined (overall grand mean). (4=100%)

Principle	Mean Pre-lab Score Raw	(%)	Mean Post-lab Score Raw	(%)	Pre-Post Score Change (in %)
I.					
(1)	3.2	(80)	3.2	(80)	0
(2)	2.0	(50)	3.8	(95)	45
(3)	2.6	(65)	3.0	(75)	10
(4)	2.4	(60)	3.8	(95)	35
(5)	2.0	(50)	3.4	(85)	35
Grand Mean	2.40	(60)	3.44	(85)	25
II.					
(6)	3.2	(80)	3.4	(85)	5
(7)	3.4	(85)	4.0	(100)	15
(8)	2.8	(70)	3.6	(90)	20
Grand Mean	3.13	(78)	3.67	(91)	13
III.					
(9)	2.6	(65)	3.6	(90)	25
(10)	3.0	(75)	3.8	(95)	20
(11)	1.8	(45)	3.2	(80)	35
(12)	3.0	(75)	3.8	(95)	20
(13)	2.4	(60)	4.0	(100)	40
Grand Mean	2.56	(64)	3.68	(92)	28
IV.					
(14)	2.6	(65)	3.6	(90)	25
(15)	2.2	(55)	3.6	(90)	35
(16)	2.2	(55)	3.8	(95)	40
(17)	0.6	(15)	2.8	(70)	55
(18)	1.2	(30)	3.2	(80)	50
Grand Mean	1.76	(44)	3.40	(85)	41

Table 10. Continued.

Principle	Mean Pre-lab Score		Mean Post-lab Score		Pre-Post Score Change (in %)
V.					
(19)	2.4	(60)	3.4	(85)	25
(20)	0.4	(10)	2.8	(70)	60
Grand Mean	1.4	(35)	3.1	(78)	+ 43
Overall Grand Mean:	2.3	(58)	3.49	(87)	+ 29

Table 11. Student pre- and post-lab scores for each interview task, total percent scores for all tasks combined (2=100%), and total percentage score change.

Task	Student 1		2		3		4		5	
	Pre	Post	Pre	Post	Pre	Post	Pre	Post	Pre	Post
1	1	2	1	2	2	2	1	2	2	2
2	2	2	2	2	2	2	2	2	2	2
3	1	2	0	1	1	2	1	2	1	2
4	2	2	0	2	2	2	0	2	2	2
5	0	1	0	1	1	2	0	2	0	2
Total % Score:	60	90	30	80	80	100	40	100	70	100
Score Change(%):	+30		+50		+20		+60		+30	

terview.

Table 12 presents mean pre- and post-lab scores for each interview task, mean score change for each task (%), and grand mean task performance scores and score change for all tasks combined. The most difficult tasks for students were tasks #5 (translation) and #3 (transcription). The grand mean score change, from 1.12 (56%) to 1.88 (94%) indicates that, on average, students were able to perform most of the tasks only partially during the pre-lab interview, but performed the tasks correctly during the post-lab interview, with minor uncertainties in reasoning and explanations still evident in some cases. Task #2 (DNA replication) was performed correctly by all students both during pre- and post-lab interviews.

Table 13 gives each student's pre- and post lab test scores (in %) on test items grouped according to major organizing principles or categories I, III, and IV. Only two test items were directly related to principles under category II, and none of the test items dealt with organizing category V. These two categories were not included in this analysis. Also shown in the table, in parentheses, are corresponding pre- and post-lab interview scores (in %) for the major organizing categories. The data show that the majority of pre-lab interview scores were lower than the corresponding pre-lab test scores, and that the difference between these scores was often large. Post- lab test and interview scores were generally much closer; about 46% of the post-interview scores were lower than the corresponding post-test scores, 40% were higher, and 14% were the same as corresponding post-test scores. Table 13 also shows each student's total % score and score change for the test and interviews. Total percent scores on interviews were almost always lower than total percent test scores. For all students, the pre-post interview score change was greater than the pre-post test score change. The reason for these results is that, whereas the multiple choice test measured primarily recall of isolated facts, concepts or propositions, the interviews measured not only these parameters, but also the relationships and linkages between a variety of concepts, propositions and principles. Student #4, for example, had a total pre-test score of 81% and a total pre-lab interview score of 42% (categories I, III and IV combined). The lower interview score does not mean that the student knew fewer isolated facts or concepts during the interview; rather, the lower score means that

Table 12. Mean pre- and post-lab scores for each interview task, mean percentage score change for each task, and grand mean scores and score change for all tasks combined. Numbers in parentheses are percentage scores (2=100%).

Task	Mean Pre-lab Score	Mean Post-lab Score	Score Change (%)
1	1.4 (70)	2.0 (100)	+ 30
2	2.0 (100)	2.0 (100)	+ 0
3	0.8 (40)	1.8 (90)	+ 50
4	1.2 (60)	2.0 (100)	+ 40
5	0.2 (10)	1.6 (80)	+ 70
Grand Mean:	1.12 (56)	1.88 (94)	+ 38

Table 13. Student pre and post-lab test scores (%) on test items grouped according to major organizing categories I, III, and IV. N= number of test items in each category. Numbers in parentheses are corresponding % scores on interviews. Also shown are total % pre-post test and interview scores and score changes for categories I, III, and IV combined.

Major Principle/ Organizing Category	Student (% Scores) 1 Pre	1 Post	2 Pre	2 Post	3 Pre	3 Post	4 Pre	4 Post	5 Pre	5 Post
I.	100	100	80	90	90	100	90	90	60	80
(N=10)	(70)	(90)	(40)	(75)	(75)	(100)	(55)	(75)	(65)	(90)
III.	83	83	33	83	83	100	83	100	83	83
(N=6)	(85)	(95)	(20)	(80)	(85)	(100)	(45)	(90)	(85)	(95)
IV.	60	100	60	40	100	100	60	80	80	80
(N=5)	(30)	(90)	(15)	(70)	(75)	(90)	(25)	(90)	(60)	(85)
Total Score out of 21:	18	20	13	16	19	21	17	19	15	17
Total % Score on Test:	86	95	62	76	90	100	81	90	71	81
Score change, %:	+9		+14		+10		+9		+10	
Total % Score, Interview (I, III., IV.):	67	92	25	75	78	97	42	85	70	90
Score Change, % (Interview):	+25		+50		+19		+43		+20	

the student did not know many of the concept linkages and propositional relationships, and/or formed incorrect linkages. The typical multiple choice test, of which the test given to the students was an example, usually does not measure such linkages and relationships. Although student #4's pre-post test score change of 9% would suggest only a small gain in overall knowledge, primarily recall of isolated facts, concepts and propositions, the pre-post interview score change of 43% indicates a substantial gain of correct concept and propositional linkages. Since the interviews measured not only more but also qualitatively different kinds of knowledge (primarily meanings and networks of conceptual relationships), a strict comparison of test and interview scores is not possible. Thus, student #4's total post-test score of 90% means that he answered 90% of the test items correctly. His post-interview score of 85% means that he knew most to all of the relevant concepts and concept relationships, with a few of the linkages still vague or uncertain (see table 9, page 33).

Table 14 shows mean pre- and post-lab test and interview scores and score changes for major organizing categories I, III, and IV, as well as grand mean scores and score changes for all three categories combined. Mean pre-lab interview scores were substantially lower than mean pre-lab test scores, although the mean post-interview and post-test scores were fairly similar. However, as suggested earlier, strict comparison of test and interview scores is not possible since interviews measure more, as well as qualitatively different, learning parameters. The table shows that the grand mean interview score change was nearly three times greater then the grand mean test score change (32% vs. 11%). The interview score change reflects a relatively large gain of correct concept and propositional linkages, as opposed to a smaller gain in isolated facts, concepts and/or propositions, as indicated by the grand mean test score change. These results suggests that responses on multiple choice test items are a much more constrained record of student learning than are responses during an interview.

Cross analysis of responses to test items and responses to interview questions involving the same concepts revealed a fairly high frequency of test-interview response discrepancies (see table 4, page 16, for discrepancy categories and explanations). Table 15 gives some actual examples of discrepancy responses for each discrepancy category. In the example for the 0+/- discrepancy category, the stu-

Table 14. Mean pre- and post-lab test and interview scores and score changes according to major organizing categories; grand mean test and interview scores and score changes for all organizing categories combined are also shown.

Major Principle/ Organizing Category	Mean Pre-lab Score(%)		Mean Post-lab Score(%)		Mean Score change (%)	
	Test	Interview	Test	Interview	Test	Interview
I.	84	61	92	86	+ 8	+ 25
III.	74	64	90	92	+ 16	+ 28
IV.	68	44	76	85	+ 8	+ 41
Grand Mean:	75	56	86	88	+ 11	+ 32

dent received no credit for his test response. The same response received some credit during the interview, since it includes a correct concept linkage, in addition to several incorrect linkages. Responses to multiple choice test items involve either/or situations. Either the student has acquired the fact or total concept meaning, or he has not.

Table 16 shows the frequency of various types of discrepancies between students' responses to test questions and their responses to similar questions during the interviews. Most of the pre-test--pre-interview discrepancies involved students being able to answer test items correctly, but having only a partial understanding (1+/-; N=19) or no comprehension (1-; N=8) of the relevant concept or proposition during the interview. This probably contributed to the lower pre-lab interview scores, relative to pre-test scores. There were also cases, although considerably less frequent, where a student answered a pre-test item incorrectly, but had a partial or complete comprehension of the relevant concept or proposition during the pre-interview (0+/- , N=6; 0+, N=2). After laboratory instruction, the frequency of discrepancies declined, from a total of 35 to a total of 18. There was a significant reduction in the type of discrepancy where a student knew the answer to a test item but had only a partial understanding or no understanding of the relevant concept or proposition. This result reflects increased comprehension of concepts and principles, and their relationships, rather than mere recall of isolated facts, concepts and/or propositions. Total post-test-post-interview discrepancies were fairly equally divided between those in which students answered test items incorrectly but had some understanding of the relevant concepts during the interview (0+,0+/-), and those in which students answered test items correctly but did not have a complete understanding of the concepts during the interview (1-; 1+/-). This probably contributed to closer agreement of post-test and post-interview scores.

Table 17 shows the frequency of pre-test-pre-interview and post-test-post-interview discrpancies arranged according to major organizing categories I, III, and IV. The same patterns observed in table 16 are apparent. The greatest number of discrepancies involved category I. This category (DNA structure; nucleotide; codon) contained facts, concepts and propositions which can be recalled with relative ease, although their interrelationships are more difficult to master and comprehend.

Table 15. Actual examples of discrepancies between test and interview responses taken from students' test and interview records. (See table 4, page 16 for discrepancy rating explanations).

Discrepancy Category/ Rating	Example
1 -	Test Response (1): The basic structure of the DNA molecule can be described as a backbone of sugars and phosphates, with nitrogenous bases bonded to the sugars. Interview Response (-): The basic structure of DNA is proteins, glucose and polymers connected to eachother.
1 +/-	Test Response (1): A DNA codon consists of a sequence of 3 nitrogenous bases. Interview Response (+/-): A DNA codon has something to do with coding. It reads in groups of 3.
0 +	Test Response (0): A DNA nuleotide consists of a phosphate and a sugar. Interview Response (+): The basic unit of DNA consists of a phosphate, sugar, and nitrogenous base, and is called a nucleotide.
0 +/-	Test Response (0): The role of messanger RNA is to carry the DNA code to the ribosomes and to determine the specific sequence of nitrogenous bases in transfer RNA, which is manufactured at the ribosomes. Interview Response (+/-): Same as above.

Table 16. Frequency of various discrepancies between test and interview responses, arranged by student. (See table 4, page 16, for explanation of discrepancy ratings/categories).

Student	Pre-Test-Pre-Interview Discrepancy					Post-Test-Post-Interview Discrepancy				
	0 +	0 +/-	1 -	1+/-	Total	0 +	0+/-	1 -	1+/-	Total
1	0	3	0	5	8	1	0	0	2	3
2	0	1	6	2	9	0	3	0	3	6
3	0	0	0	3	3	0	0	0	1	1
4	0	1	2	5	8	0	2	0	2	4
5	2	1	0	4	7	3	1	0	0	4
Grand Total:	2	6	8	19	35	4	6	0	8	18

Table 17. Frequency of various discrepancies between test and interview responses arranged according to major organizing principle/category.

Major Organizing Category	Pre-Test/Interview Discrepancy					Post-Test/Interview Discrepancy				
	0+	0+/-	1-	1+/-	Total	0+	0+/-	1-	1+/-	Total
I.	1	2	3	9	15	1	3	0	5	9
III.	2	2	0	6	10	1	0	0	1	2
IV.	0	2	4	3	9	1	3	0	2	6

Discussion

The primary purpose of this study was (1) to evaluate and compare the effectiveness of interviews and multiple choice tests as learning assessment tools, specifically, the kind of learning these techniques assess, and (2) to determine the effect of laboratory instruction on students' comprehension of molecular genetics as revealed by pre- and post-lab test and interview scores. The results show that the interviews were very effective in revealing the variety of students' conceptual-propositional linkages, missing concepts and misconceptions. Two basic patterns emerged from interview analysis: (1) certain concepts, propositions and principles of molecular genetics were missing from a large proportion of the students interviewed, and (2) misconceptions were remarkably idiosyncratic. Missing concepts can be attributed to a number of factors, including degree of difficulty and specificity of the concepts, lack of adequate related anchoring concepts in student cognitive structure, quality of instruction (introductory lecture), lack of effort, committment or reflective thinking by the student to learn the concept or concept set. The last factor was partly controlled during the experiment by asking students not to review lecture or laboratory notes prior to pre- and post-lab tests and interviews.

The interviews showed that a major pre-lab missing concept was the concept of the nucleotide as the basic structural unit of DNA, mRNA and tRNA. Failure to recognize the nucleotide as the basic unit of these three interdependent molecules caused students to treat these molecules as isolated, unrelated entities, rather than as related structures participating in the common goal of protein synthesis. A common pre-lab missing principle was the relationship between DNA (genotype), RNA, protein synthesis and phenotype. This crucial organizing principle was mentioned only briefly during the introductory lecture, although it may be the single most important advance organizer and superordinate principle in molecular genetics. It subsumes and defines the overall purpose of all subsidiary principles and processes comprising the Central Dogma of molecular genetics. The pre-lab interviews showed that one of the main reasons for students' difficulties with the conceptual relationships in molecular genetics was

their lack of comprehension of the overall purpose and result of the various processes in molecular genetics (replication, transcription, translation). Without an all-inclusive meaningful organizing principle such as the DNA-RNA-protein synthesis-phenotype relationship, students had no effective way of organizing and integrating the various concepts, propositions and principles into a meaningful network of related concepts.

Missing concepts and inadequately differentiated concepts contributed to misconceptions or invalid linkages between different concepts and different propositions. The striking variety of idiosyncratic misconceptions resulted from the unique ways in which students linked various concepts together in an attempt to place these concepts into relationships that made some sense. In most cases, misconceptions resulted from inadequate differentiation of component concepts in a proposition or principle. For example, the misconception that "adenine and thymine are different genes" is attributable to inadequate differentiation of the concepts of gene, nucleotide and nitrogenous base. The prevalent pre-lab misconception that "DNA has amino acids in it" probably stemmed from a confusion between nucleic acids and amino acids. This concfusion is understandable on the basis of inadequate differentiation of nucleic and amino acids. DNA and RNA are nucleic acids. Amino acids, on the other hand, are "carried by" tRNA and are ultimately united into proteins at the ribosomes.

The meaning that a student expresses in an erroneous proposition may not be a misconception to the student. This is particularly true if the student is satisfied that his interpretation of the conceptual relationship makes some sense, despite uncertainties that may exist in his mind, due to inadequate differentiation of component concepts. In such instances, the misconception has a functional meaning, as appeared to have been the case for student #4's pre-lab interpretation of the translation process (figure 4A, page 30). Most of his concept linkages were incorrect, leading to numerous false propositions. The student attempted to make sense out of concepts and concept labels which were inadequately differentiated. Although he had relatively little to work with other than a set of nebulous concept labels, he devised a scheme whereby protein synthesis would be accomplished entirely within the cell nucleus. Inadequate differentiation of concepts such as tRNA, mRNA and ribosomes forced him to create his own meaning-

ful relationships to explain the translation process. The student did not know or consider that the volume of the cell nucleus is too small to accomodate the large number of proteins continually produced by a cell, and that severe osmotic imbalances would result from packing proteins into the nucleus. Subsequent clarification and further differentiation of these concepts during the laboratory exercise resulted in the complete elimination of these misconceptions (figure 4B, page 30).

The post-lab interviews showed that laboratory instruction resulted in a significant reduction in the number of missing concepts and misconceptions. The primary reason for this was greater differentiation of concepts, propositions and principles, leading to clearer and more meaningful conceptual linkages. Students generally had a better understanding of the overall relationship between DNA (genotype)-RNA-protein synthesis-phenotype. It is likely that this superordinate principle helped them to organize their concepts and to draw correct relationships between the various subsidiary principles, propositions and concepts included under DNA structure, replication, transcription and translation. The importance of such superordinate principles in organizing students' thinking has been stressed by a number of educational researchers and learning theorists (Ausubel, 1968; Novak, 1980; Novak and Gowin, 1984; Stewart, et.al., 1979).

Several concepts and propositions related to the type and strength of bonds connecting the DNA strands were still missing or were interpreted incorrectly even after laboratory instruction. There was a rather persistent view that the hydrogen bonds connecting the DNA strands had to be strong. This idea persisted despite previous instruction that hydrogen bonds are, by nature, weak bonds, and that DNA strand separation is required for replication and transcription. Interview responses suggest that this misconception may have been caused by a metaphysical bias or common sense theory (Hill, 1983) that structures must be held together as tightly as possible in order for them to maintain their structural integrity. Several students commented that the DNA strands had to be tightly bonded to prevent them from "coming apart". This is an interesting inconsistency since these same students realized that the strands had to separate during replication and transcription.

Unlike the interviews, the multiple choice test used in this study did not detect the divergent idiosyncratic meanings, incorrect propositions and incorrect propositional linkages held by the students

before and after the laboratory exercise. The test did not discriminate between missing concepts and misconceptions. Interpretation of student responses on such a test requires making a whole set of assumptions as to why a student chose one response over another. The test revealed only which isolated concepts, propositions or principles the student knew or did not know and, by itself, did not determine whether the student comprehended the concepts or had learned them merely verbatim. The inadequacy of the test in making the distinction between missing concepts, misconceptions, verbatim recall,and comprehension was shown by the analysis of discrepancies between test and interview responses.

Comparison of students' pre- and post-lab interview scores on comprehension of concepts, propositions, principles and their relationships showed that students made significant gains in these areas following laboratory instruction. Students also made substantial gains in their comprehension and interpretation of various processes in molecular genetics, as shown by higher post-lab scores on interview tasks. Scores on the multiple choice test rose only slightly after the laboratory exercise, reflecting relatively small gains in recall of isolated concept meanings, propositions and principles. Pre-lab interview scores were substantially lower than pre-lab test scores (mean score difference of 19%). Although this difference is partly an artifact of test-interview scoring scale differences, it does indicate that, whereas students were able to recall isolated concepts, concept meanings, propositions and processes on the pre-lab test, they did not know or comprehend their relationships during the interviews. Consequently, pre-lab test scores generally were not reliable indicators of meaningful learning or comprehension of test items and the subject matter in general. Sole reliance on pre-lab test scores as indicators of levels of comprehension would have overestimated the students' understanding of molecular genetics.

Post-lab interview and test scores were in fairly close agreement, with a mean score difference of only 2%. Overall, this indicates that students' comprehension of concepts and principles "caught up" with their recall of isolated concepts and principles. Test scores (organizing principles I, III, and IV) rose by a mean of 11%, which translates to a mean increase of 2.3 correct responses an the post-lab test. Interview scores rose by a mean of 32% after the laboratory exercise. This increase must be interpreted in relation to the mean pre-lab

interview score, which was 56%. This score indicates that, on average, students had 50-75% of the concepts and principles, with a mix of missing, incorrect, correct, and vague concept linkages, prior to the laboratory exercise. The mean post-lab interview score increase of 32% indicates that, on average, students gained an additional 10-15% of the total pool of concepts after the laboratory exercise and, more significantly, that missing and incorrect concept linkages were almost entirely replaced by correct and/or slightly uncertain linkages. The mean post-lab test and interview scores were 86% and 88%, respectively. These scores are not strictly comparable since the scoring scales were not identical, and also because the scores imply different learning and evaluation parameters. The post-lab test score means that, on average, students answered 86% of the isolated test items (18/21) correctly. The post-lab interview score means that, on average, students knew most of the concepts (about 80-90%) as well as the correct linkages between the relatively large number of concepts, propositions and principles of molecular genetics. It can be argued, therefore, that whereas the pre-lab test scores tended to overestimate students' knowledge and comprehension of molecular genetics, the pre-post lab test score gains, and the final post-lab test scores tended to underestimate the gains students had made in comprehending the complex network of conceptual relationships in molecular genetics.

The results of the analysis of discrepancies between test and interview responses raises questions regarding the validity of multiple choice tests as tools for assessing comprehension and meaningful learning. Novak and Gowin (1984) have suggested that there is often little correspondence between students' responses to multiple choice test items and the meanings students express during interviews. The findings in this study support this view. Students frequently were able to answer isolated test items correctly without being able to explain the meaning of the relevant concepts, or their relationship to other relevant concepts, during the interviews. Several students commented that they were able to answer certain test items by a process of elimination. Some choices apparently served as cues leading the student to the correct answer. Makers of multiple choice tests try to eliminate this problem by incorporating subtle distractors among test-item choices. When these distractors become too subtle, students frequently complain that the test item is "tricky". In many instances, these complaints may be legitimate, and the process of evaluation is reduced to the level of who

can outwit or outguess whom. Novak (1981) classified most multiple choice tests as notoriously non-discriminating, due to inherent ambiguities and subsequent misinterpretation of questions and choices by the student. In this study, this problem may have partly contributed to the type of test-interview discrepancies whereby students answered certain test items incorrectly but had either a partial or complete comprehension of the relevant concepts or proposition during the interview. Such discrepancies, whatever their causes, indicate that a multiple choice test can underestimate student knowledge and comprehension. Analysis of student scores or responses to certain test items will not reveal what the student actually knows or does not know, if the test item (1) is ambiguous, (2) fails to test for meaningful conceptual relationships, which the student may actually know, or (3) concentrates on factual recall or discrimination between subtly different valid and invalid conclusions.

Although test-item flaws may have contributed to some of the test-interview response discrepancies in this study, the significant reduction in the total number of discrepant test-interview responses following the laboratory exercise suggests that the main factor responsible for the high frequency of pre-test-pre-interview discrepancies was the students' lack of comprehension of concepts, principles and their relationships. The laboratory exercise provided opportunities to clarify these relationships, with subsequent reduction of post-test-post-interview response discrepancies.

Conclusions - Implications for Research and Teaching

The results of this study have specific implications for learning and teaching of molecular genetics, as well as implications for learning, teaching and educational research, in general. The amount of data generated by interviews regarding student comprehension of concepts and principles in molecular genetics was substantially greater than information gained from test scores and responses. Pre-lab interviews showed that students had only a minimal understanding of the relationships between general principles in molecular genetics. This is shown schematically in Appendix 4A. The desired learning outcomes for a unit in molecular genetics are shown in appendix 4B. Neither the introductory lecture, which was a regularly scheduled component of the introductory biology course, nor the laboratory exercise in molecular genetics (Appendix 2), attempted to integrate the principles of molecular genetics with critical related concepts such as mitosis, meiosis, DNA recombination and sex cell formation. These subjects were treated separately in earlier lectures and laboratory exercises. The results of this study tend to suggest that students learn concepts and principles meaningfully when they are linked to other related, relevant concepts and, particularly, when subsidiary concepts and principles are subsumed and organized under higher-order, more inclusive principles. Consequently, student learning and comprehension of molecular genetics, mitosis, and meiosis could probably have been significantly improved had these concepts and principles been presented together as a unit.

The results of this study lead to the following specific conclusions:

1. Interviews were effective in revealing student pre- and post-lab missing concepts and misconceptions in molecular genetics.
2. The multiple choice test did not discriminate between missing concepts and misconceptions.
3. The interviews and interview tasks revealed the meanings students attached to concepts and sets of related concepts by the types of conceptual and propositional linkages students formed.
4. Students were generally missing the same concepts or sets of concepts before laboratory instruction, but misconceptions were highly idiosyncratic. The same pattern was observed after the laboratory exercise, except that

the number of missing concepts and misconceptions declined.

5. The post-lab interviews and interview tasks showed a substantial gain in meaningful conceptual linkages and differentiation of concepts.
6. The multiple choice test measured student knowledge of isolated concept meanings and propositions rather than knowledge of relationships between concept sets and principles comprising the conceptual network of molecular genetics.
7. The multiple choice test did not discriminate between rote recall and comprehension.
8. Pre-lab test scores were higher than pre-lab interview scores, reflecting students' abilities to recall isolated concepts and concept meanings on the test, without being able to explain their relationships and overall meaning during the interviews.
9. Post-lab test and interview scores were higher than pre-lab scores, and were similar. The similar scores do not reflect the same learning parameters. Gains on the post-lab test reflect gains in isolated factual knowledge or concept meanings. Gains on post-lab interview scores reflect not only gains in factual knowledge, but also gains in conceptual cross linkages and meaningful learning (comprehension).
10. Cross analysis and discrepancies between test and interview responses showed that pre-lab test scores overestimated comprehension levels, wheras post-lab test scores tended to underestimate student comprehension of conceptual relationships in molecular genetics.
11. Discrepancies between pre-lab test and interview responses were common and may have been the result of a combination of factors including (a) ambiguous, non-discriminating or easily discriminable test questions and choices (b) interviewing techniques (ambiguous questions and/or arrangement of questions leading to suggested responses) (c) students' feelings towrds test taking and interviewing. Some of these factors are difficult to control. Most of the discrepancies were caused by students answering isolated test items correctly, without being able to properly explain their meaning and relation to other relevant concepts during the interviews. Discrepancies between test and interview responses declined significantly after the laboratory exercise.
12. The decline in the number of test-interview response discrepancies after the laboratory exercise suggests that the main cause of discrepancies was lack of clear understanding of concepts, principles and their relationships.

Educational researchers interested in investigating meaningful learning, conceptual relationships and misconceptions should consider using individual student interviews rather than multiple choice tests as learning assessment tools. It is doubtful if a multiple choice test can be constructed in a way that would provide the type, quantity and quality of data required to assess students' meaningful integration and comprehension of concepts and conceptual relationships in a given subject matter. Robinson (1979) suggested that there is no sure way to ascertain if responses on a multiple choice test reflect verbatim recall or higher cognitive processes. According to Novak (1981), most multiple choice tests do not give a clear indication of meaningful learning and are too easily structured to require only rote, nonsubstantive recall of information. The results of this study tend to support these conclusions.

For classroom teachers, student interviews would be a desirable way of assessing student knowledge prior to instruction, so that subsequent teaching can address missing concepts and misconceptions from the students' perspectives. However, interviews are time-consuming and would be difficult to incorporate logistically into the usual classroom setting. A number of researchers have suggested the use of concept maps in learning and teaching, as a valid alternative technique for externalizing the concept meanings and relationships held by students (Novak, 1979; Novak, 1980; Novak, 1981; Novak and Gowin, 1984; Stewart, et.al., 1979). Novak and Gowin (1984) present methods wherby concept maps can be used as learning and teaching tools, and scored for evaluation purposes.

More research is needed on the possible causes of discrepancies between test and interview responses. Since it is likely that multiple choice tests will be a part of the educational evaluation scene for some time, such research may lead to better methods of test construction, in addition to refinement of interviewing techniques. Data generated by improper interviewing techniques (ambiguous questioning, suggested responses) is just as unacceptable as data generated by improperly constructed multiple choice tests.

In summary, the results of this study suggest, in general, that the choice of learning, teaching and research methodologies (interviews, concept mapping, objective tests) involves making choices among various learning objectives and teaching-learning philosophies. The results of this study indicate that if meaningful lear-

is to be the primary target of a particular educational research or classroom teaching-learning event, an objective paper-and-pencil test is not likely to provide the necessary information to determine whether or not meaningful learning has taken place.

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APPENDICES

Appendix 1.

Pre/Post Test

1. DNA is found in the:
   (a.) cell nucleus
   b. cell cytoplasm
   c. ribosomes
   d. endoplasmic reticulum

2. DNA is most closely associated with:
   (a.) chromosomes
   b. vacuoles
   c. the plasma membrane
   d. ribosomes

3. The basic structure of the DNA molecule can be descibed as:
   (a.) a backbone of sugars and phosphates, with nitrogenous bases bonded to the sugars
   b. a backbone of sugars and nitrogenous bases, with phosphates bonded to the nitrogenous bases
   c. a backbone of phosphates and nitrogenous bases with sugars bonded only to the nitrogenous bases
   d. a backbone of sugars and amino acids, with nitrogenous bases bonded to the sugars

4. (True) or False: A DNA molecule is a double-stranded molecule

5. Circle all functions performed by the DNA molecule:
   a. production of ATP
   (b.) carrying genetic information
   (c.) production of RNA
   (d.) supplying genetic code for protein synthesis
   (e.) involved in chromosome replication during mitosis and meiosis
   f. production of glucose in dark reaction of photosynthesis

6. When a DNA molecule replicates, separation of the original molecule occurs between the:
   a. sugar molecules
   (b.) nitrogenous bases
   c. phosphates
   d. amino acids

7. Briefly explain what is meant by "complimentary base pairing" in the DNA molecule

8. A DNA nucleotide consists of:
   a. two phosphates
   b. a phosphate and a sugar
   (c.) a sugar, phosphate and nitrogenous base
   d. two sugars and a nitrogenous base

9. A DNA codon consists of:
   (a.) a sequence of 3 nitrogenous bases
   b. a sequence of 3 sugars
   c. a sequence of 2 nitrogenous bases
   d. a sequence of 4 nitrogenous bases

Appendix 1. Continued.

10. What is the significance of the sequence of codons in a DNA molecule?
    a. it determines the amount of ATP generated in the Krebs cycle
    (b.) it determines the sequence of nitrogenous bases in messenger RNA, which will determine the sequence of amino acids in proteins manufactured at ribosomes
    c. it determines the sequence of sugars in messenger RNA which determines the sequence of amino acids in proteins
    d. the sequence of codons is random and has no significance; only the individual codons are important in specifying the type of protein made at the ribosomes

11. Each DNA codon specifies a particular:
    a. protein
    b. enzyme
    (c.) amino acid
    d. ATP molecule

12. What is meant by transcription of the DNA code?
    (a.) the code is transferred to RNA during its manufacture by a DNA strand
    b. the code is duplicated when DNA divides
    c. the code is transferred to mitochondria to initiate ATP production
    d. the code is used to initiate mitosis

13. What is the role of messenger RNA?
    a. it carries the DNA code to the mitochondria to initiate ATP synthesis
    (b.) it carries the DNA code to the ribosomes and determines the sequence of amino acids in the manufacture of specific proteins
    c. it carries the DNA code to the ribosomes and directs the synthesis of specific transfer RNA molecules
    d. it carries the DNA code message to the cell membrane and directs the passage of proteins into and out of the cell

14. What is the role of transfer RNA molecules?
    a. they transfer proteins from the nucleus into the cytoplasm of the cell
    (b.) they carry specific amino acids, which they transfer to messenger RNA at the ribosomes
    c. they carry specific proteins, which they transfer to the messenger RNA at the ribosomes
    d. they transfer ATP and proteins from the mitochondria to the ribosomes and endoplasmic reticulum

15. Circle all statements which apply to both messenger and transfer RNA molecules:
    (a.) they are manufactured in the nucleus
    (b.) the sequence of their nitrogenous bases is determined by the base sequence of the DNA strand from which they are made
    (c.) they are single-strand molecules
    (d.) they take part in protein synthesis
    e. they are found only in the nucleus of the cell
    (f.) they are found in the nucleus, cytoplasm and ribosomes

16. Which one of the following statements best describes the function of ribosomes?
    a. they are the sites of ATP synthesis, during which messenger and transfer RNA join up at the ribosomes and determine the amount of ATP produced
    b. they read the code message of messenger RNA and then pull in transfer RNA molecules with their specific amino acids and proteins
    c. they read the code message of messenger RNA and then pull in transfer RNA molecules with their specific amino acids
    (d.) they read the triplet codes of messenger RNA and pull in transfer RNA molecules with complimentary triplet codes and specific amino acids
    e. they read the triplet codes of messenger RNA and pull in transfer RNA molecules with complimentary triplet codes and specific proteins

Key: Question #7: A specific nitrogenous base always pairs up with one other, specific nitrogenous base. Adenine-Thymine Cytosine-Guanine, in DNA. In RNA: Adenine-Uracil Cytosine-Guanine

Test Questions Grouped According To Major Organizing Principles as Shown in Table 2, page 8-9

Category	Test questions pertaining to category	
I	1, 2, 3, 4, 5b, 5d, 7, 8, 9, 11	N=10
II	5e, 6	N=2
III	5c, 10, 12, 15a, 15b, 15c	N=6
IV	13, 14, 15d, 15f, 16	N=5

Appendix 2. Laboratory Exercise on Molecular Genetics.

Bio 1 - Laboratory #9

MOLECULAR BIOLOGY

The objective of this laboratory is dual: 1) to study the structure of deoxyribonucleic acid (DNA) and ribonucleic acid (RNA), and the processes of replication, transcription, and translation (protein chain formation), and; 2) provide a broad overview of the basic techniques used in the study of nucleic acids, and make the student aware of the potential and uses of genetic engineering in all relevant disciplines.

The first objective is achieved through the use of three exercises dealing with two-dimensional models: a) DNA: The Genetic Code; b) RNA: The Code Transcribed; and 3) Protein Synthesis: The Code Translated. The purpose of these 3 exercises is to summarize the central dogma of molecular biology:

To avoid detracting from this primary goal, most of the details concerning enzyme activity, energy requirements, and other factors associated with replication, transcription, and translation are omitted.

A film dealing with nucleic acid techniques is used to achieve the second objective of this lab. In the film the techniques are demonstrated at the laboratory bench so that the student acquires a true feel for the techniques and practical difficulties involved. With the aid of suitable experimental examples, the demonstration of techniques is organized so as to resemble a coherent scientific investigation in molecular genetics. The student will realize the relationship of each technique to each other and how the variety of techniques can be used as a whole towards a defined scientific objective.

Finally, research materials related to the general subject of this lab will be demonstrated to the students.

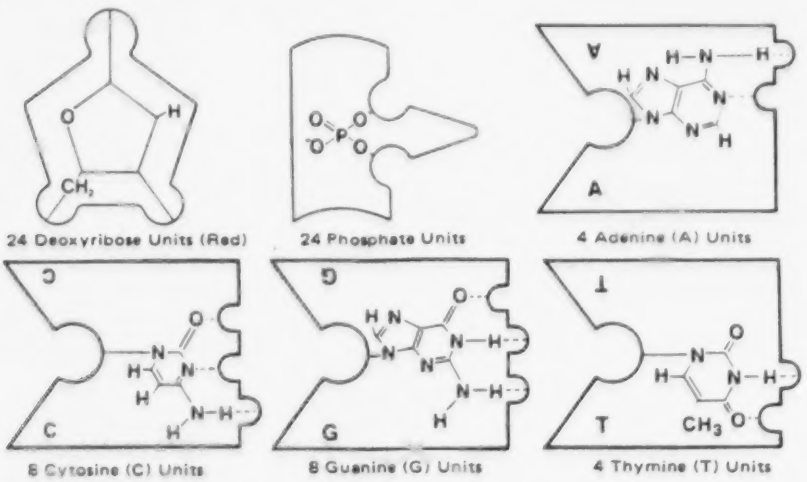
Note: Permission for inclusion and reproduction of the Student Worksheet in molecular genetics (DNA Puzzle Kit, Cat. # 17-1050) was granted by Carolina Biological Supply Company (Jan. 5, 1987).

Student Worksheet **Name** _____

DNA: The Genetic Code **Date** _____

Nucleic acids are long, chainlike molecules formed by the linking together of smaller molecules called nucleotides. A nucleic acid, deoxyribonucleic acid or DNA, is the material which comprises the gene.

Obtain the following pieces for your team. During the exercise, always keep the printed side of each piece up.



THE DNA NUCLEOTIDES. Examine a deoxyribose unit. Deoxyribose is a sugar. The three knobs represent covalent chemical bonds which deoxyribose can form with the bases and phosphate. The molecule consists of a ring of four carbon atoms and one oxygen atom. Individual carbon atoms are not shown, but are located at the intersections of lines. To one side of the oxygen atom is a carbon atom bonded to a CH_2 group. Attach a phosphate unit to the free bond that comes from the CH_2 group. On the opposite side of the oxygen atom is a carbon atom with a free bond shown. Attach an adenine base to this bond. The structure now represents an adenine nucleotide. The representation is incomplete: The adenine nucleotide is a triphosphate, not a monophosphate as shown by your representation. The two additional phosphate groups are removed during DNA synthesis. The phosphate end of the molecule is referred to as the 5′ end. The as yet unused covalent bond comes from the 3′ end of the molecule. Put together the rest of the deoxyribose, phosphate, and base units to form additional nucleotides. After all the nucleotides have been assembled, set aside one-half of each type nucleotide for later use in DNA replication.

COVALENT BONDING OF NUCLEOTIDES. Select an adenine nucleotide and a guanine nucleotide. Join them by connecting the phosphate unit of one to the free carbon bond of the other. Continue adding nucleotides in this manner until you have built up a strand of 6 nucleotides as shown in Figure 1. The actual linkage of nucleotides is an enzyme controlled process which involves splitting off phosphate groups as noted above.

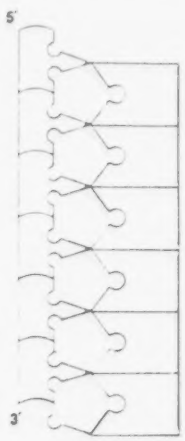


Figure 1

BASE PAIRING. Select one of the remaining nucleotides and attempt to pair it with a nucleotide of the strand by putting the ends of their bases together. Attempt several such pairings using different bases. Then fill in the following: Adenine pairs only with _____. Cytosine pairs only with _____.

Bases which will pair are said to be complementary. The bonds between the bases are not covalent bonds, but much weaker *hydrogen bonds*.

DNA STRUCTURE. Duplicate figure 2 by pairing each nucleotide of the first strand with its complementary nucleotide and joining the bonds to form a new strand. Notice that the two strands are antiparallel (they run in opposite directions); that is, if one strand runs 5′ to 3′ (phosphate-sugar, phosphate-sugar) from top to bottom, the other must run 3′ to 5′ from top to bottom. The structure which is produced represents the double-stranded DNA molecule. Using A, C, G, T indicate on Figure 2 the base sequence which you have produced for each side of the molecule.

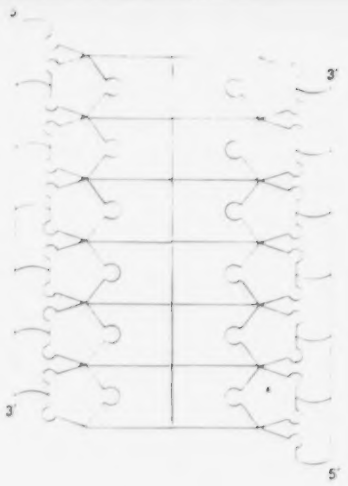


Figure 2

THE GENETIC CODE. The sequence of bases in DNA forms a code or set of instructions for protein synthesis. Each code word or *codon* consists of a sequence of three bases and specifies a particular amino acid. There are 64 possible codons (Fig. 3). Some are chain terminating codons which are not known to specify any amino acid. These indicate where a protein chain is to end. In most cases, an amino acid can be specified by more than one codon, but each codon can specify only one amino acid. Usually one strand (the sense strand) of DNA is active in protein synthesis. The codons of the inactive or antisense strand are not used in protein synthesis. Consider the right side of the molecule that you have constructed to be the sense strand and read the codons from the 3′ end of the strand toward the 5′ end. Which amino acids are specified by the two codons? _____ and _____ .

DNA CODON 3′–5′	AMINO ACID SPECIFIED
ATT ATC ACT	CHAIN TERMINATING
CGA CGG CGT CGC	Alanine
GCA GCG GCT GCC TCT TCC	Arginine
TTA TTG	Asparagine
CTA CTG	Aspartic Acid
ACA ACG	Cysteine
GTT GTC	Glutamine
CTT CTC	Glutamic Acid
CCA CCG CCT CCC	Glycine
GTA GTG	Histidine
TAA TAG TAT	Isoleucine

DNA CODON 3′–5′	AMINO ACID SPECIFIED
AAT AAC GAA GAG GAT GAC	Leucine
TTT TTC	Lysine
TAC	Methionine
AAA AAG	Phenylalanine
GGA GGG GGT GGC	Proline
AGA AGG AGT AGC TCA TCG	Serine
TGA TGG TGT TGC	Threonine
ACC	Tryptophan
ATA ATG	Tyrosine
CAA CAG CAT CAC	Valine

Figure 3

DNA REPLICATION. Separate the two DNA strands to a distance of about 30 cm. The weak hydrogen bonding between the base pairs allows for this separation. From the free nucleotides left on your work space, rebuild the missing half of each DNA strand. Begin at the 3′ end of the original strand and proceed to its 5′ end. Compare the base sequences of the new molecules to the base sequence of the original molecule as recorded on Figure 2. Has the original base sequence been maintained during replication? _____ .

REVIEW. Repeat the above procedures until you are familiar with DNA structure and replication.

Carolina Biological Supply Company Burlington, North Carolina 27215
Gladstone, Oregon 97027
CB211098110

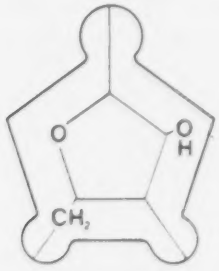
Student Worksheet
RNA: The Code Transcribed

Name _____

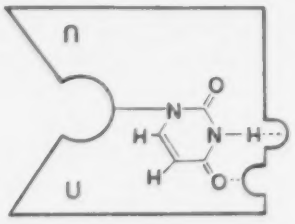
Date _____

RNA is produced by using DNA as a pattern. During this process, called transcription, the genetic code is transferred from DNA to RNA.

Obtain the following units for your team: 12 Deoxyribose (Red), 12 Ribose (Pink), 24 Phosphate, 4 Adenine (A), 8 Cytosine (C), 8 Guanine (G), 2 Thymine (T), 2 Uracil (U). During the exercise, always keep the printed side of each piece up.



12 Ribose (Pink)



2 Uracil (U)

NUCLEOTIDES. Compare a deoxyribose unit to a ribose unit. Look at the formula of each molecule as printed on the units. How does deoxyribose differ from ribose sugar? _____

_____ .

The nucleotides of DNA contain deoxyribose sugar while nucleotides of RNA contain ribose sugar.

Use the deoxyribose units to form the following DNA nucleotides: 2 adenine, 6 cytosine, 2 guanine, and 2 thymine. Now use the ribose units to form the following RNA nucleotides: 2 adenine, 2 cytosine, 6 guanine, and 2 uracil.

TRANSCRIPTION. During transcription the two strands of a DNA molecule become separated along part of the molecule's length. One strand of DNA remains inactive, but the other, the sense strand, is used to bring about the synthesis of RNA. To demonstrate transcription, first use the deoxyribose nucleotides to form a single strand of DNA. We will use this as the sense strand and ignore the antisense strand. Beginning at the 3′ (sugar) end of the strand, pair each DNA nucleotide with its RNA complement (uracil of RNA complements adenine of DNA) and link together the phosphate and ribose units to form a strand of RNA. (Notice that RNA synthesis begins at the 5′ end of the RNA strand and proceeds toward its 3′ end.) Separate the RNA and DNA strands. Once RNA is formed, it is released from DNA and goes to other parts of the cell. How does transcription differ from replication? _____

_____

_____

TYPES OF RNA. Transcription produces three major types of RNA: ribosomal (rRNA), transfer (tRNA), and messenger (mRNA). Ribosomal RNA combines with proteins to form bodies called ribosomes. The ribosomes become located in the cell's cytoplasm and are centers for protein synthesis. Transfer RNA reacts with amino acids in the cytoplasm and interacts with ribosomes and messenger RNA in the assembly of amino acids into proteins. It is messenger RNA that brings the instructions for protein synthesis (the genetic code) from DNA in the nucleus to the ribosomes.

MESSENGER RNA AND THE GENETIC CODE. Look again at the sense strand of DNA and the RNA strand produced by it. Notice that the sequence of bases in RNA is controlled by the sequence of bases in DNA; that is, the RNA codons (triplets of bases) are complementary to the DNA codons. Figure 1 gives the possible DNA codons with their corresponding mRNA codons and the amino acids specified by each. (In the table, the mRNA codons are read from the 5' end of the molecule to the 3' end.) Which amino acids are specified by the RNA strand that you have assembled?

_____, _____, _____, and _____

DNA CODON	mRNA CODON	AMINO ACID SPECIFIED
ATT ATC ACT	UAA UAG UGA	CHAIN TERMINATING
CGA CGG CGT CGC	GCU GCC GCA GCG	Alanine
GCA GCG GCT GCC TCT TCC	CGU CGC CGA CGG AGA AGG	Arginine
TTA TTG	AAU AAC	Asparagine
CTA CTG	GAU GAC	Aspartic Acid
ACA ACG	UGU UGC	Cysteine
GTT GTC	CAA CAG	Glutamine
CTT CTC	GAA GAG	Glutamic Acid
CCA CCG CCT CCC	GGU GGC GGA GGG	Glycine
GTA GTG	CAU CAC	Histidine
TAA TAG TAT	AUU AUC AUA	Isoleucine

DNA CODON	mRNA CODON	AMINO ACID SPECIFIED
AAT AAC GAA GAG GAT GAC	UUA UUG CUU CUC CUA CUG	Leucine
TTT TTC	AAA AAG	Lysine
TAC	AUG	Methionine
AAA AAG	UUU UUC	Phenylalanine
GGA GGG GGT GGC	CCU CCC CCA CCG	Proline
AGA AGG AGT AGC TCA TCG	UCU UCC UCA UCG AGU AGC	Serine
TGA TGG TGT TGC	ACU ACC ACA ACG	Threonine
ACC	UGG	Tryptophan
ATA ATG	UAU UAC	Tyrosine
CAA CAG CAT CAC	GUU GUC GUA GUG	Valine

Figure 1

REVIEW. Repeat the above procedure until you are familiar with the process of transcription.

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CB211108110

Student Worksheet
Protein Synthesis: The Code Translated

Name _____

Date _____

Messenger RNA (mRNA) and transfer RNA (tRNA) work together to position amino acids at the ribosome for protein synthesis. The kinds and numbers of amino acids used are determined by the mRNA codons; thus, the genetic code is translated into a sequence of amino acids during protein synthesis.

Obtain the following units: 12 deoxyribose, 12 ribose, 24 phosphate, 2 alanine tRNA, 2 glycine tRNA, 2 alanine, 2 glycine, 2 alanine activating, 2 glycine activating, 4 adenine (A), 8 cytosine (C), 8 guanine (G), 2 thymine (T), and 2 uracil (U). Also obtain a ribosome template. During the exercise always keep the printed side of each piece up.

TRANSCRIPTION. Use the deoxyribose units to form the following DNA nucleotides: 2 adenine, 6 cytosine, 2 guanine, and 2 thymine. Now use the ribose units to form the following RNA nucleotides: 2 adenine, 2 cytosine, 6 guanine, and 2 uracil.

Use the deoxyribose nucleotides to form a single strand of DNA identical to that shown in Figure 1. The base sequence (beginning at the 3′ end of the molecule) should be CGT, CCA, CGT, CCA as shown. Now transcribe a strand of mRNA from the DNA strand.

TRANSFER RNA. Each tRNA molecule (there is a different tRNA for each kind of amino acid) consists of about 75 nucleotides. One loop of the molecule has three unpaired bases that are complementary to one of the codons of mRNA. These three bases (called an anticodon) are shown magnified at the top of the tRNA units. One end of the tRNA molecule terminates in the nucleotide sequence CCA. An activating enzyme can attach an amino acid to the terminal A nucleotide of the tRNA. The enzyme is specific for a particular amino acid and for a particular tRNA. Thus, the amino acid glycine can only be attached to a tRNA specific for glycine.

Attach each of the activating units to the amino acid unit for which it is specific. Then attach each activating unit-amino acid complex to a tRNA unit.

PROTEIN SYNTHESIS. Position the mRNA on the mRNA binding site of the 40 S subunit of the ribosome template. The 5′ (phosphate) end of the mRNA should be to the right as indicated on the sheet. Pick up a tRNA-amino acid unit whose anticodon complements the mRNA codon above the P site of the 60 S subunit and place it on the P site with codon and anticodon paired. Do the same for the A site.

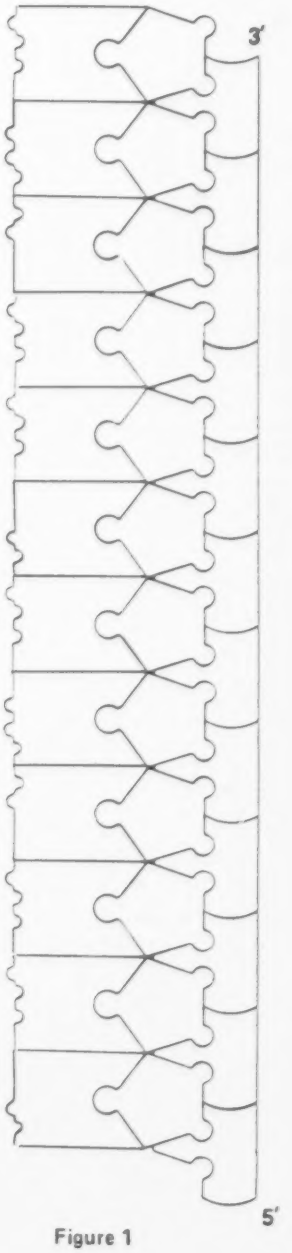

Figure 1

Detach the P site amino acid from its tRNA-activating unit and slide it over the tRNA, attaching it to the A site amino acid. Move the mRNA to the right until the tRNA-activating unit amino acid chain occupies the P site (the tRNA-activating unit amino acid chain is moved from the A site to the P site). Carefully lift the empty tRNA-activating unit complex, slide it out from under the amino acid chain, and place it to one side. Fill the A site with another tRNA-amino acid unit and repeat the above process until you have produced a chain of the four amino acid units. Then fill in Table 1.

TABLE I

DNA CODONS (3′ END)		mRNA CODONS (5′ END)		AMINO ACIDS IN PROTEIN CHAIN
CGT	→	_____	→	_____
CCA	→	_____	→	_____
CGT	→	_____	→	_____
CCA	→	_____	→	_____

Suppose you had started with the DNA codons CGT, CCA, CCA, CGT. How would this have affected the outcome? _____

_____

_____

REVIEW. Repeat the above procedure until you are familiar with protein synthesis.

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Appendix 3.

Portion of pre-laboratory interview for student #2.

I: Is there a relationship between RNA and DNA?
R: Their structure is pretty much the same, except RNA has uracil instead of thymine. Otherwise, the bases are the same.

I: Do you know how RNA is made, Tom?
R: No, I dont know that.

I: Can you think of any relationship between DNA, RNA and protein synthesis?
R: It happens in the ribosomes, but I don't know how. DNA is only in the nucleus and RNA is only at the ribosomes.

I: O.K., here we have a single strand. Can you tell me what it is?
R: I think it's DNA. You have thymine there, not uracil, so I think it's DNA, not RNA.

I: Look at these units. Do you think they're RNA or DNA units?
R: I don't know. Some of the chemicals look different than the ones in the strand of DNA. I guess they must be RNA units because some of them have uracil.

I: Can you take some of those units and build a second strand, using the DNA strand as a model?
I: Now you have a double strand again. What is it?
R: I think it's RNA because you have uracil.

I: You think both strands are RNA?
R: Yes, I think so.

I: But what about this thymine, here? Shouldn't that be uracil if this is RNA?
R: Yes, but there's uracil in the other strand. I'm not sure.

I: Are you saying that if you have uracil in one strand but thymine in the other, both strands are still RNA?
R: I'm not sure. I think so.

I: Is there a relation between RNA and ribosomes?
R: Ribosomes store energy and proteins. I think there is a synthesis of proteins at the ribosomes to get energy and RNA is involved.

I: What are proteins made of?
R: Amino acids.

I: What determines the difference between one protein and another?
R: The structure inside them.

I: Can you tell me the nature of the structure?
R: I think there is a primary and secondary structure and amino acids.

I: O.K., Let's go back to this double strand and separate it into two strands. Can you do that?
I: We've separated the double strand down the middle. We now have two single strands. What are they?
R: RNA

I: Do you know if RNA/DNA is involved with what goes on at the ribosomes?
R: I know that RNA is involved because its ribonucleic acid. The ribo- stands for ribosome.

I: What goes on at the ribosomes?
R: Proteins and amino acids are changed into something, probably RNA.

I: Are there different kinds of RNA?
R: Yes, mRNA and transfer RNA.

I: Where in the cell are they found?
R: I think they're both at the ribosomes.

I: What do they do there?
R: They have something to do with the make-up of proteins.

I: Is there a difference between mRNA and tRNA?
R: tRNA brings something in, because of the word "transfer". mRNA tells the order of bases or the type of protein. It carries some sort of message.

I: You said that mRNA tells the order of bases and carries a message. Can you explain that further?
R: I'm not sure. I think the order of bases determines different proteins. It's the message.

I: Where and how are these different proteins made?
R: They're made at the ribosomes. I'm not sure how they're made.

I: But you did say that mRNA is involved, right?
R: Yes. It carries the message.

I: What about tRNA? Does it have something to do with making proteins?
R: I think so, but I don't remember what it does.

I: Let's get back to one of these single strands of RNA. Can you tell me what a codon is or point one out to me on this strand?
R: I don't know what that is.

I: Do you know the significance of a combination of any three of these units? (nucleotides/nitrogenous bases)
R: No.

I: What about a genetic code? Do you know what that is and if there is one in this RNA strand?
R: It's genetic information carried by DNA. I'm not sure if there's a code in RNA.

I: What does the genetic information in DNA stand for?
R: Amino acids and proteins, I think. I remember hearing something like that.

Portion of post-laboratory interview for student #2.

I: Can you tell me how RNA is related to DNA?
R: It's a single strand, I believe.

I: How is RNA made?
R: I'm not sure.

I: Well, tell me what you know about RNA, what it does, the types of RNA.
R: There's transfer and messanger RNA. mRNA goes to the cytoplasm with a message and tRNA reads it and interprets it.

I: What sort of message does mRNA carry?
R: Genetic information.

I: What does this genetic information stand for?
R: I'm not sure.

I: O.K., then, where does RNA get its message or genetic information?
R: From the pairing of bases or codes.

I: From the pairing of bases or codes. What bases or codes?
R: I'm not sure.

I: O.K., does the term "transcription"ring a bell?
R: Yes. It's the taking of genetic information and placing it so that RNA can be made.

I: I see. But what makes the RNA? Do you remember what we did in lab?
R: No, I'm not sure.

I: Here we have a single strand. Do you know what it is?
R: RNA (Note: the strand was DNA)

I: Why do you say that?
R: Because it's a single strand. Oh no, it must be DNA because if it were RNA it would have uracil instead of thymine. It must be a single strand of DNA.

I: Do you remember from lab how DNA functions in transcription?
R: I think it involves something moving across and pairing up with respective bases and that would make a chemical that would be the base of the RNA.

I: That would make a chemical that would be the base of the RNA. What do you mean by that? Can you explain that some more?
R: What you get is another DNA so you get a double-stranded DNA. No, wait. But if you have uracil here you would get RNA. Oh, so it would be RNA.

I: So, what you're doing now is assembling an RNA? (R is asked to assemble RNA from available nucleotides)
R: Yes. From the DNA strand.

I: Is the whole molecule RNA? Both strands?
R: I'm not sure. I think just the one on the right. (the one assembled)

I: So, can you repeat again what we mean by transcription?
R: It's making an RNA strand from DNA.

I: In what part of the cell does this all take place?
R: In the nucleus. mRNA comes to the nucleus to read DNA.

I: What about the amino acids? What happens to them?
R: They will make only certain chemicals, such as glycine or alanine.

I: Are you saying that glycine and alanine are chemicals made by amino acids?
R: Yes, I think so.

I: But earlier you pointed out that glycine and alanine were amino acids.
R: Oh, what I meant to say is that tRNA creates amino acids.

I: I see. Let's take a look at this alanine tRNA and this glycine tRNA. Let's try to match them up to the mRNA. Why does the alanine tRNA fit here, and not the glycine tRNA?
R: Because the mRNA base order GCA can only create alanine, not glycine.

I: What you are saying now, then, is that a certain base order of mRNA creates certain amino acids, such as alanine?
R: Yes, I think so.

I: But earlier you said that tRNA creates certain amino acids.
R: I'm not really sure. I think that mRNA gives a message to tRNA to create an amino acid.

I: I see. Let's go on. We have here two tRNA molecules hooked up to the mRNA. What happens next?
R: I don't really know. I just remember from lab something breaking off and sliding down. I think the Amino acids have to separate from the tRNA to create proteins--they have to come together. But I don't remember exactly how we did it.

I: O.K. Can you tell me what determines the types and the order of amino acids that are put together?
R: The codons of tRNA and mRNA. They're both involved in making proteins. A certain codon in mRNA will satisfy only a certain tRNA codon.

I: I see. Can you tell me the name of the process during which all of this takes place?
R: Translation

I: Can you tell me how all of the things we've been talking about take part in determining what an organism looks like, its phenotype? What determines what <u>you</u> are and what you look like?
R: The DNA, genes and different chromosomes. The different proteins make people look different.

Portion of pre-laboratory interview for student #4.

I: Can you tell me what RNA is?
R: It codes for DNA.

I: How is RNA made?
R: Somehow from DNA.

I: What happens to RNA after it is made from DNA?
R: I'm not sure. mRNA reads what DNA says.

I: What's the ultimate purpose of this?
R: It gets amino acid groups to latch on to mRNA to put together a chain of amino acids to form proteins.

I: Can you tell me the relationship between the sequence of bases in DNA and RNA?
R: There's no set order, but the bases pair up in a special way.

I: O.K., here we have a single strand. What do you think it is, and why?
R: It's DNA. It has thymine, not uracil.

I: What about these loose units here, what do you think they are?
R: I don't know, but in some of them, they have uracil. There are no thymine units.

I: How might we put these units together and what will they form?
R: They're going to latch on to DNA and then make a full DNA molecule--maybe not a DNA molecule, I don't know what it's called--a DNA structure maybe.

I: Are we then repeating what we did earlier in the DNA replication process?
R: Yes, I think so...but without thymine.

I: But earlier you said that these units have uracil instead of thymine; what sort of strand has uracil and not thymine?
R: RNA. So we're going to make RNA from DNA.

I: Let's try to do that with the available units here. How are you going to put them together?
R: By pairing the bases in the units with the DNA strand bases.

I: So now we have a double strand again. What is it?
R: It's RNA.

I: Are you saying that both strands now are RNA?
R: Maybe not. I think just the second one. The first one is still DNA. The DNA is used to make the RNA.

I: And what determines the sequence of bases in the RNA?
R: The DNA sequence.

I: The DNA sequence. What sequence in the DNA?
R: The bases.

I: O.K., can you tell me what the sequence of RNA bases stands for?
R: It brings an amino acid.

I: Can you point out a codon on this RNA strand?
R: I don't know what that is. It has something to do with coding the whole thing.

I: Well, what happens to this double strand now?
R: It's going to separate in the middle.

I: O.K. we've separated the strands. What's important about the sequence of RNA bases and what do they correspond to?
R: They correspond to the sequence of DNA bases. It's going to create a chemical, an acid or a protein.

I: What's going to create a chemical?
R: The information in the mRNA. The bases and nucleotides. tRNA will read the information and this creates an acid or protein.

I: Are you saying that the bases and nucleotides in the mRNA represent some kind of information?
R: Yes. Each group of three bases is a codon.

I: What does a codon stand for?
R: They create a specific chemical. I think they code for amino acids and proteins.

I: O.K. let's go back to this mRNA strand here. What happens to it now?
R: It goes from the nucleus to the ribosome.

I: What happens to it at the ribosome?
R: It carries the message from DNA in the nucleus. It will change when it gets to the ribosome.

I: Change to what?
R: To tRNA. Oh no, I think it will be worked on by tRNA in some way.

I: Can you explain that further?
R: I think tRNA will read across different bases and codons and when it has read a certain sequence it will stop.

I: What's the ultimate purpose of all of that?
R: To create proteins, which are made up of polypeptide chains and amino acids.

I: Where do the amino acids come from?
R: Three bases make a codon which codes for an amino acid. I think the codon creates amino acids and they come together to make proteins. tRNA reads so many acids and then stops when it has gotten what it wants for the protein.

I: O.K. let's move on. Do you recognize this? (ribosome template)
R: It's a model of a ribosome.

I: What's going to happen to the mRNA strand we made?
R: It goes to the ribosome.

I: Please show me how this happens, Tom.
I: O.K., what happens now?
R: t RNA is going to read the mRNA.

I: Can you show me the tRNA molecules in this group?
I: O.K., what are some things you notice about these tRNA molecules?
R: They bond to amino acids.

I: O.K., now what is the tRNA going to do now, in relation to mRNA?
R: It's going to give the genetic code. It's going to come in and read the mRNA and then it will break off.

I: Well, let's look at this RNA strand. Can you tell me how many amino acids will be coded for by this strand? (12 bases/nucleotides)
R: 4. Because it codes in groups of 3.

I: Groups of three, what?
R: Bases.

I: In what part of the cell is RNA made or put together into a strand?
R: Mainly in the nucleus. Maybe also in the cytoplasm.

I: Can you give me two major types of RNA?
R: mRNA and tRNA.

I: Can you explain any differences between these two?
R: I think tRNA is smaller than mRNA. tRNA is made from mRNA, I think.

I: Is that all?
R: That's all I remember.

I: O.K., let's assume this strand we've made here is mRNA. What happens to it now?
R: It goes along the DNA strand and reads it and when it gets to a certain point it stops and degenerates.

I: Are you saying that it stays on the DNA strand and just reads it?
R: Yes.

I: O.K., then, where do the amino acids come in?
R: They're attached to the mRNA. After the mRNA reads the DNA, the amino acids will connect and then mRNA will go on to the next one. The amino acids will stay to form a chain, to get a protein.

I: What is the mRNA reading?
R: The DNA bases, in groups of three.

I: Are you saying that mRNA stays with the DNA and reads the codons, and then amino acids are put together?
R: Yes.

I: And where did you say the amino acids come from?
R: They're on the mRNA.

I: Are you familiar with ribosomes and how they function in this process?
R: Ribosomes are on the mRNA and read it.

I: What do they read?
R: They read for DNA. They're connected with the mRNA, I think, and they read for DNA. Then, amino acids are brought in by the mRNA to which they're connected, like the ribosomes. You could say that the amino acids are "on the back" of the mRNA molecule.

I: O.K., but earlier you said that mRNA reads the DNA. Now you're saying that ribosomes on the mRNA actually read the DNA. Can you explain this further?
R: I think the ribosomes help to read the DNA, together with the mRNA.

I: Well, do you know where tRNA fits into this process?
R: I don't really know. I think it gets the mRNA with its amino acids to the DNA to read it.

Portion of post-laboratory interview for student #4.

I: Can you explain to me the relationship between RNA and DNA and how they work together?
R: RNA is a single strand made from a DNA strand. The DNA splits and RNA forms from it. It reads the DNA message and codes for amino acids that will be brought over by tRNA.

I: In what part of the cell is RNA manufactured?
R: In the nucleus.

I: What happens to the mRNA after it is made in the nucleus?
R: mRNA is made from DNA and reads it. Then it goes to the ribosomes. tRNA brings in amino acids and hooks up with mRNA. Eventually the amino acids will latch together to make proteins.

I: O.K., here we have a single strand. What is it, and why?
R: DNA, because there is thymine, not uracil.

I: What about these free units, here? What do you think they are?
R: RNA units with thymine..no, uracil instead of thymine.

I: Do you know what we mean by transcription?
R: The reading of the DNA chain by RNA.

I: Can you now use these units to make a strand of RNA?
I: O.K., how did you construct that RNA strand?
R: By matching the RNA bases with the proper DNA bases.

I: So, what determines the base sequence of RNA?
R: The sequence of DNA bases.

I: And why is this sequence important?
R: It determines the kinds of amino acids put together to make a certain kind of protein.

I: What kind of RNA did you make here?
R: mRNA.

I: What happens to it now, and where does it go?
R: It has to separate from the DNA and then it goes to the ribosomes where it is read for protein synthesis.

I: What reads it?
R: The ribosomes and the tRNA.

I: Tell me what you know about tRNA.
R: It has a free codon which hooks up to a mRNA codon. It carries amino acids. It's also made from DNA, I think.

I: How do mRNA and tRNA work together and what's the ultimate outcome?
R: Well, tRNA comes in with its codon and pairs with the bases of the mRNA. It carries amino acids. It leaves the amino acids and then goes off. The amino acids hook up together to form proteins.

I: O.K., can you tell me where tRNA is usually located and where it gets its amino acids?
R: It's usually in the cytoplasm and this is where it picks up amino acids which it brings to the ribosomes to make proteins with the mRNA.

I: O.K., do you recognize this from lab? (ribosome template)
R: A ribosome.

I: What about these units here? (tRNA)

R: They're tRNA's with amino acids, like glycine or alanine.

I: O.K., let's go back to the mRNA strand we made earlier. Can you show me what has to happen to it now?

R: It has to separate from the DNA strand and go to the ribosome.

I: We now have the mRNA strand located at the ribosome. What happens now?

R: tRNA comes in with an amino acid. The tRNA has to match up with the right mRNA base triplet. Then another tRNA comes in next to the first one. The amino acids detach from the tRNA and hook together. Then the mRNA shifts over and another tRNA can come in. The first tRNA goes away. The first two amino acids hook up with the third one. Then a protein is formed. The process can repeat itself many times to form the needed protein.

I: Can you explain to me the difference between phenotype and genotype?

R: Genotype is your genetic information in DNA and this determines phenotype or appearance.

I: O.K., but what is it, precisely, that the genetic information or DNA of each organism does which makes the organism look different from other organisms?

R: It makes different kinds of proteins. It's the different proteins in different animals that make them look the way they are.

Portion of pre-laboratory interview for student #5.

I: Do you know something about the relationship between RNA and DNA?
R: RNA has something to do with protein synthesis, because you have mRNA and tRNA.

I: Do you know how RNA is made?
R: It must be from DNA. It has something to do with translation and transcription.

I: Can you explain the difference between transcription and translation?
R: Transcription is making RNA from DNA. Translation is how amino acids are made and put together by the code in mRNA.

I: Can you give me some more details about transcription and translation, particularly in regard to mRNA?
R: mRNA runs along the DNA strand and from this you get triplets of nitrogen bases and from that you pick up your amino acids and they are hooked up together.

I: Are the amino acids hooked up in some kind of order or just randomly?
R: I think in an order.

I: And what determines this?
R: I think the mRNA.

I: Can you explain that a little more?
R: I think the genetic material in mRNA is in an order and this shows the order of amino acids.

I: Can you tell me something about the relationship between mRNA and tRNA and how they work together?
R: The triplet bases are located on mRNA and somehow they align with tRNA and there's one case where the message stops when it hits something.

I: What do the triplet bases in mRNA stand for?
R: Amino acids.

I: What is it that carries the amino acids and how are they put together?
R: Probably the tRNA. It follows along the mRNA somehow, that's all I know.

I: O.K. here we have a single strand put together and there are some free units scattered next to the strand. Can you tell me what the strand is and the free units next to it?
R: The strand is DNA. It has thymine. The free units might be RNA because some of them have uracil. Some of the chemicals also have a different color.

I: Earlier you said that we can make RNA strand from DNA. Can you do this using these units, here?
I: O.K., you put together another strand. Can you explain what you did?
R: I matched up the bases. Guanine with cytosine, and adenine in DNA with uracil in RNA.

I: Now, is the whole double-strand an RNA or a DNA?
R: The original strand is still DNA and the other one on the right is an RNA strand.

I: What controls the sequence of bases in the RNA strand?

R: The sequence of DNA bases.

Portion of post-laboratory interview for student #5.

I: What do we mean by transciption?
R: How DNA gets to be RNA.

I: How is RNA different from DNA?
R: It has uracil instead of thymine and is a single strand.

I: What determines the sequence of bases in RNA?
R: The sequence of bases in DNA.

I: Where does transciption take place?
R: I think in the nucleus, maybe also at the ribosomes.

I: O.K., Karen, here we have a single strand. What do you think it is, and why?
R: It's DNA because it has thymine instead of uracil.

I: What are these units here next to the strand?
R: RNA units. They have different sugar and there is uracil instead of thymine.

I: O.K., using the single DNA strand, can you now use these units to build a second strand?
I: Now we have a double-strand. What is it?
R: There's the DNA strand and the RNA strand which we put together.

I: How did you build that RNA strand up, using the DNA strand?
R: I paired up the bases.

I: What are the two major types of RNA?
R: mRNA and tRNA.

I: Is the strand you built mRNA or tRNA?
R: I don't know. I think it could be either.

I: O.K., let's assume this is mRNA. What happens to it now?
R: It has to separate from the DNA. It then goes from the nucleus to the ribosomes. The ribosomes read it.

I: What is it about the mRNA that the ribosomes read?
R: The base sequence. It dictates amino acids.

I: And what determines the base sequence in mRNA?
R: The base sequence of DNA.

I: And where do the amino acids come from?
R: They're floating around, and according to the codons on mRNA, they're going to attach to mRNA and eventually they're united into proteins.

I: Where does this protein building take place?
R: At the ribosomes.

I: O.K. Earlier you said that the RNA has to separate from the DNA before it goes to the ribosomes. Let's do that now.
I: Now we have this single strand of RNA. Do you recognize this? (ribosome template)
R: A model of a ribosome.

I: What happens to this RNA now?
R: It goes to the ribosome.

I: O.K. Let's do that. Are we dealing here with mRNA or tRNA?
R: m RNA.

I: O.K. The mRNA is now at the ribosome. How are amino acids brought to the ribosome?
R: By tRNA.

I: Are you saying that tRNA carries amino acids?
R: Yes, I think so.

I: Can you pick out some tRNA molecule models here?
I: O.K. what does the alanine and glycine represent here on these tRNA molecules?
R: They're amino acids.

I: Eventually, what do these tRNA molecules have to hook up to?
R: A codon on the mRNA.

I: O.K. here we have a GCA mRNA codon. What tRNA codon/anti-codon would hook up with it?
R: CGU.

I: Can you show me now, using these models and from what we did in lab, how mRNA and tRNA work together at the ribosome.
I: O.K. you did quite well with that. What's the name of this entire process and what is the ultimate purpose?
R: Translation. It's to build a protein chain from amino acids.

I: Where do you think tRNA goes after giving up its amino acid?
R: Back to the nucleus? I don't know. Eventually they pick up an amino acid again and go through the proccess again.

I: Ultimately, when we say that DNA determines what you look like and how you function---what do we really mean by this?
R: I think it's that some different proteins are produced by the different DNA of each individual and this accounts for differences.

Portion of post-laboratory interview for student #3.

I: Can you tell me the relationship betweenRNA and DNA?
R: RNA is made from DNA. DNA gives genetic information to RNA which copies the DNA information. The DNA splits, mRNA comes in and copies the code from one of the DNA strands. It uses uracil instead of thymine. The mRNA then takes the code and carries it to the ribosomes in the cytoplasm. Then tRNA comes along and mRNA has a certain code, which is a series of codons. A codon is three nitrogen base units. mRNA gets this code from the DNA. tRNA has opposite codons that hook up with the mRNA codons. tRNA also carries amino acids. It waits for another tRNA, which hooks up to the next mRNA codon. Now, the amino acids hook together, the first tRNA drops off and gets another amino acid. Another tRNA comes along with another amino acid and that amino acid hooks on to the other amino acids until you get a polypeptide or protein chain.

I: From what you just said, Tony, what is the ultimate purpose of the DNA genetic code?
R: The production of different proteins or enzymes.

I: You said that DNA gives genetic information to RNA and that mRNA comes in to copy the DNA code. Can you explain that further?
R: Actually, mRNA is made from a strand of DNA.

I: I see. Is there a name for that process?
R: It's transcription.

I: And where does this take place?
R: In the nucleus. This is where mRNA is given a code by DNA for protein production. Translation takes place at the ribosomes. This is where the code is translated into amino acids and proteins with the help of tRNA.

I: O.K., here we have a single strand. What is it and how can you tell?
R: DNA. It's got thymine instead of uracil.

I: Can you now make a mRNA strand using these nucleotides?
I: O.K., you now made another strand. How did you determine the sequence of nucleotides and bases in the RNA?
R: By pairing the bases up with the complimentary DNA bases.

I: Now what happens?
R: The mRNA strand separates from the DNA strand and goes to the ribosome with the code. This is where translation occurs.

I: O.K., let's do that. Can you pick out the ribosome and tRNA molecules at this station?
I: O.K., what do you notice about the tRNA?
R: They carry amino acids which they pick up in the cytoplasm.

I: Let's place the mRNA strand on the ribosome....What determines which tRNA with its amino acid will hook up to the GCA mRNA codon?
R: The tRNA with the CGU anticodon will join with the complimentary GCA mRNA codon. This brings in alanine. The next tRNA is carrying glycine. The alanine separates from the tRNA and hooks to the glycine and then the first tRNA breaks away. The process is repeated over and over again with different tRNA's coming in until a protein chain is formed.

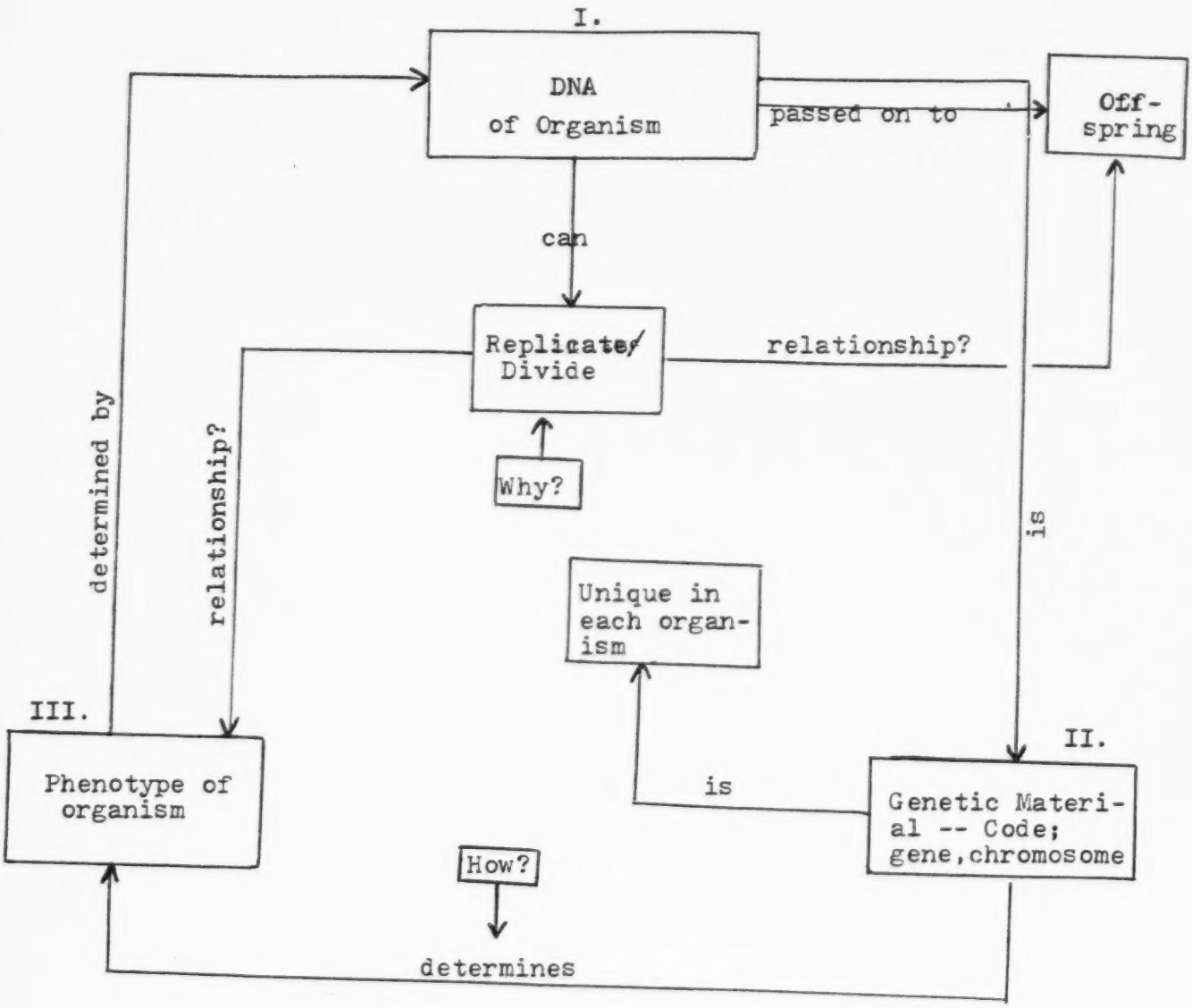
I: What has to happen to the mRNA strand in order to accomodate all the different tRNA's?

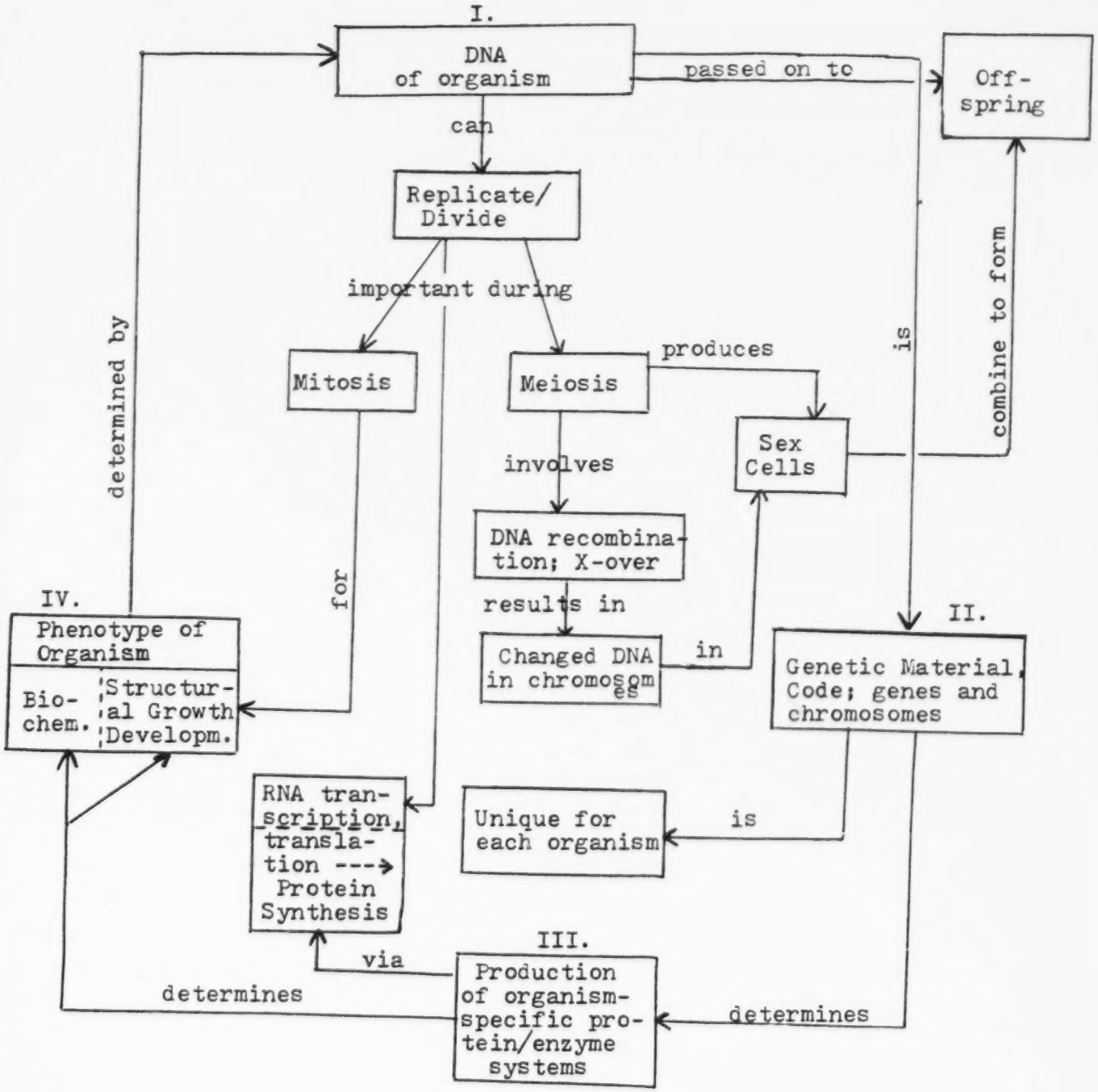
R: It has to shift or move along the ribosome. Actually, it's the ribosome that's moving. It reads the mRNA like a ticker-tape machine and pulls in the proper tRNA's to hook up with the mRNA codons.

I: We're doing quite well here, Tony. Do you know what is meant by phenotype and how it is determined?

R: It's all the chemical reactions that go on in the body and how things are put together to make you look the way you do. It's determined by the kinds of proteins and enzymes in your body, which goes back to the kind of DNA you have.

Appendix 4A. Schematic representation of general relationships in molecular genetics most likely held by students prior to laboratory instruction or in-depth discussion of topics related to the Central Dogma in Molecular Genetics.





Appendix 4B. Desired learning outcomes for topics related to Central Dogma in molecular genetics.